U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

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ve a special meaning. G	ive examples or	r relevent cita	tions, authors,	keywords, etc., if k	nown. For sequen	e any · ces,
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Structure

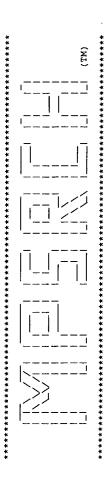
Bibliographic

DARC/Questel

Other

PTO-1590 (9-90)

Number of Databases:



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Thu Feb 18 14:40:49 1999; MasPar time 2624.06 Seconds 1532.792 Million cell updates/sec abular output not generated. no un

>US-08-934-254-26 (1-1702) from US08934254.seq 1702 Description: Perfect Score: N.A. Sequence: Comp: Title:

TABLE default Gap 6 Scoring table:

602357 seqs, 1181590623 bases x Searched:

Dbase 0; Query 0

Nmatch STD:

Minimum Match 0% Listing first 45 summaries Post-processing:

emb157 Database:

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_or 15:em_vi 9enbank110 16:gb_bat 17:gb_baz 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov 22:gb_pat 23:gb_ph 24:gb_pl1 25:gb_pt 23:gb_pr 23:gb_pr 29:gb_ro 30:gb_st 31:gb_st 33:gb_vi 34:gb_vi

Mean 11.427; Variance 5.921; scale 1.930

tatistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		ap (
No.	Score	Match	Watch Length DB	3 10	Description	Pred. No.
1	399	23.4	110149 2	5 ATAC005397	Arabidopsis thaliana c	4.77e-288
7	393	23.1	1705 2	5 ATAJ4161	Arabidopsis thaliana m	
m	385	22.6	1610 2	5 BNAJ4160	Brassica napus mRNA fo	1.22e-276
4	340	20.0		5 HACYTB5RN	H.annuus mRNA for extr	4.63e-240
ß	172	10.1		2 AR020904	Sequence 4 from patent	1.78e-105
ø	172	10.1		2 I38430	Sequence 4 from patent	1.78e-105
7	172	10.1	1687 2	5 BOU79010	Borago officinalis del	1.78e-105
∞	91	5.3		2 I66494	Sequence 14 from paten	2.20e-43
σ	46	2.7		2 AR024229	Sequence 22 from paten	7.60e-12
10	43	2.5	281 24	4 RYERNRA	Secale cereale nitrate	6.13e-10
11	42	2.5	10772 1	9 AF012089	Drosophila melanogaste	2.59e-09
c 12	40	2.4	965 23	2 AR024229	Sequence 22 from paten	4.48e-08
13	40	2.4	10772 19	9 AF012089	Drosophila melanogaste	4.48e-08

2.92e-06 7.36e-07 2.92e-06 1.14e-05 4.41e-05	4.41e-05 4.41e-05 1.14e-05 4.41e-05	1.67e-04 1.67e-04 6.22e-04 6.22e-04 2.27e-03	6.22e-04 8.15e-03 8.15e-03 8.15e-03 2.86e-02	2.86e-02 2.86e-02 2.86e-02	9.84e-02 9.84e-02 9.84e-02 9.84e-02 9.84e-02
000	Hordeum lechleri nitra Hordeum pusilium nitra Zea mays nitrate reduc C.maxima nitrate reduc Hordeum vulgare nar? g	V.carteri gene for nit Sequence 5 from patent Rice nial gene for nit Hordeum bogdanii nitra Hordeum stenostachys n Maize NADH:nitrate red	L.japonicus NIA gene. Avena strigosa nitrate CDNA encoding cytochro gDNA encoding envelope Human mucin Z (MUC2) m Homo sapiens intestina	Human Chromosome 11p12 *** SEQUENCING IN PROG Homo sapiens chromosom C vilgaris mBNA for ni	Streptomyces coelicolo Genorhabditis elegans Caenorhabditis elegans Homo sapiens 12924 PAC *** SEQUENCING IN PROG
166494 AC005369 AC005369 128278 BLYNRB	BLYNRC BLYNRD MZENADHNR CUCNITRA HVNAR7	VCNITA 128278 OSNIA134 BLYNRA BLYNRF	LJNIA ASTNRA E13060 E04076 HUMIMUCA HUMMUC2X	AC003025 AC004228 AC004063	SC2EL CEY47H9C CEY53C10 AC004216 AC005921
22 27 22 24	44444	404444	762244	27 27 27	178 178 178 178
7218 74371 74371 215 285	285 285 1801 3076 3538	7602 215 2000 282 285 285	5499 273 540 565 3811 15720	112309 170743 177014	38962 75342 110000 181098 231298
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14 15 17 18	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	32225	3 3 3 3 3 5 1 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	338	4443
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family=".(TAAAA)n"
complement(14264...14323)
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complement(14412. .15176)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(<5548. .>7570)
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complement(12493. .12)
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                                                                                                                                                                                                                                     The property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identified by repeatmasker (Arian Smit, Arian Smit, Sepanan Smit, Spename, Washington, edu/RM/Repeatmasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="KLMSINEKRSLGTIWSPANVCCVQFSSYSNHLLAFGSADYKVYC
SLDRKYVTRWCTLAGHEKRAVSYVKFNDSETIVSASTDNSLKLWNLNKTNSSGLSFGAC
SLTYKGHTNOKNFVGLSVLDGYIACSSETNEYYSYKSLPMPWTSYKFGSVDPISGNE
YFDDNGQFVSSVCWRKKSNMLVAANSTGNMKLLKLV"
                                                                                      Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene
                                   The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1464. 1565

//note="exon predicted by xgrail, quality excellent"
complement(1490. 1522)
//note="exon predicted by xgrail, quality
marginal_shadowexon"
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/gene="T3F17.2"
4337. .5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality marginal"
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/note="exon predicted by xgrail, quality good"
complement(3773. .3849)
4087. .4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(<1. .21,180. .497,585. .644,805. .>996)
/gene="T3F17.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="putative Cop1 protein, 5' partial"
'db_xref="PID:93702316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="T3F17.1"
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//note="exon predicted by xgrail, quality
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4106. .4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     excellent_shadowexon
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the YAC clone CIC02E07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="CIC02E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .110149
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Sperling, P., Zaehringer, U. and Heinz, E. Identification of cDNAs coding for a sphingolipid desaturase from
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Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                    TAGAGAACCGCCGCGAGCATGACGCCGACGCACGTGAGTGTGTAAAGAGTCACGTGACCT 45697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45875 TTGAGAATCGCTGCTTCGCCTCCGGGATGAGATTTAACCCAATCGGAAACGTCGTAAACT 45934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
     45458 ATTGAGATGCCGGTGAGACAGTTACCGGAGAGAAGCTGGATTAGTTTGTTACACGGTTTG 45517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45758 ACGTCTGACACGTGGTGGTCTCTCACGT-G-A-TAGCCATTGTGAAGCTTTTCTAAGTGG 45814
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                                                                                                                                      196 CTGAGGAGGGGACCTCGCCGCGGGTGCTCCGCCGCCCACCGAGAGCAGTCGTAGACC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLN 31-OCT-1998 sphingolipid desaturase
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                                                                                                                                                                                                                                                                            496 AAGCCCAGCAGTGCGCCGCAGAGCATGTGAACTCCGACGGACTCCGACGCCAGCACGCCG
                                                                                                                                                                                                                             AGACCGAGTAAAACGGCGGAGATGAGGTGAGCCCAGATGCTGGTACACGCCAAAACGCCG
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                                                          ATGCTGATTCCGGTTAGGATGTTGCCTGCTATGAGTTGCGTGATTCTGTTGTATCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-8 sphingolipid desaturase; fusion protein; sld1 gene thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45935 TTACCTTGAATCGAAATCCATAAATCTCCAGGTTTGTTGTG 45975
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/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAJ4161 1705 bp mRNA
Arabidopsis thaliana mRNA for delta-8
AJ224161
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17042. .17131,17227. .17313,17401. .17480,17583. .17768)
/gene="T3E17.6"
/gene="T3E17.6"
                                                                                                                                                                                                                                                                                                                                          join(15955. 16138,16274. 16489,16586. 16719,16820. 16939,
17042. 17131,17227. 17313,17401. 17480,17583. 17658)
/gene="TJF17.6"
                                         //db_xref="PID: g3702319"
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MLAVNLRCGGVSLNKLDTDSPKCILNTLWYKIISN"
//translation="MADYQMPKCTTT"
//translation="Madyquad"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 399; DB 25; Length 11
Pred. No. 4.77e-288;
0; Mismatches 400; Indels
/note="hypothetical protein"
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Best Local Similarity 67.3%;
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Brassica napus
Bukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae;
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                                                                                               AACTICGCCGGAATCITAGICITCIGGACTIGGITCCCACICITAGICICAIGICIACCA
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 TTCAACTCCATCACCTCGGTCTTCTATGGCCGAGTCCTGAAATTCGACGAAGTGGCACGG
                                 TICTTAGTCAGCTATCAACACTTTACTTATTATCCAGTTATGTGCCTTTGGAAGAATCAAT
                                                 AACTGGCCTGAGAGATTCTTCTTCGTCTTCACAAGCTTCACCGTCACGGCGCTTCAACAC
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Brassica napus mRNA for delta-8 sphingolipid desaturase.
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sequence: X87143.
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GDTVILNLVGQDYTDAFIAFHFGTAWHILDHLFTGYHIRDEOVSEVSRDYRRAAAEFR
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ADVYVGPPTGSDWFRRAMFELVSTSYMDKLFGLIGGFILKRVS
PYVQELCKKHNLPYRSMSWFFANVLTINTLKTAAYQARDVANPVVKNLVWBALNTHG"
parts, some flowers, few roots'
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'tissue_type="mainly green
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Matches 808; Conservative
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Pred. No. 1.22e-276;
0; Mismatches 407;
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gene="sld1"
                       /gene="sld1"
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llarity 66.7%;
Conservative
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Best Local Similarity
Matches 828; Conser
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domain - desaturase-like
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common sunflower.
Helianthus annuss
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotyledons; Asteridae; Asterales; Asteraceae;
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TITCCTCTTTTAGTATCCTTCCTACCAAACTGGCAAGAGGATCATCTTTGTCTTTTTA
                                                                                                                                                                                   AGCATGGCCGTCACGGCGATTCAGCACGTTCAGTTCTGTTTAAACCATTTTGCGGCAGAT
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/cell_type="embryonic storage"
/clone="PCR-CDNA"
1. 1591
73. 1449
/note="N-terminal cytochrome b5 domain - desaturas
                                                                   AGACGTTACGTTCCTGATCGAGCCTTGAACATAGCTGGGATTCTTGTTTTCTGGACGTGG
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Submitted (10-MAY-1995) P. Sperling, Univ Hamburg, Inst.
Allgemeine Botanik, Ohhnorstzr. 18, 22609 Hamburg, FRG
Related sequences: AJ224160, AJ224161.
Location/Qualifiers
1. 1591
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/cultivar="inbred line HA89, sf163
/db_xref="taxon:4232"
/dev_stage="21 DAF"
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Sperling, P., Schmidt, H. and Heinz, E.
A cytochrome-b5-containing fusion protein lipid desaturases
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H.annuus mRNA for extraplastidial
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US-08-934-254-26.rge

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1228 CACCATTTGTTTCCTAGGTTGCCACGGTGTCACTTGAGGTCGATTTCTCCTATATGTAGA 1287
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                996 AGCTTTGCGGTCACGGCGATCCAGCACGTCCAGTTCACGCTCAACCACTTCTCCGGCGAC
                                                                                                                                                                                                       1168 GATATCGCGTGTTCTTGGATGGATGGTTTTTCGGAGGTTTACAGTTTCAACTTGAG
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AAACGAAAGATTCCCGACAGAGGTTTAAACATACTCGGAACCCTAATCTTCTGGACGTGG
                                                             TTTCCGTTACTTGTTTCTCGCTTACCGAACTGGCCCGAACGCGTGGCGTTTGTTGTGTTGGTT
                                                                                                                        1048 AGCTICTGTGTAACGGGTATACAACATATTCAGTTTACACTGAACCATTTTTCTGGGGAT
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Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and
Freyssinet,G.L.
Production of gamma.linolenic acid by a .DELTA.6-de
Patent: US 5789220-A 4 04-AUG-1998;
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Pred. No. 1.78e-105;
0; Mismatches 507;
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1. .1685
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277 c 357 g
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4 from patent US
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1 Similarity 57.7%;
697; Conservative
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                                                      TEMARTH PROGRAPLINIAGOUY TARKETKKHNNPNDLMISILGKYYNY
TEWAKRHPGGDAPLINIAGOUY TARFHFOTAWKHLDKLFTGYHLKDYQVSDISRD
TEWAKRHPGGDAPLINIAGOUY TARFHFOTAWKHLDKLFTGYHLKDYQVSDISRD
TEKLASERFAKANFEKKHGYISILSCYSLLLSACYVGVLTSGSFWIHLMLSGALIGLA
WMQIAYLGHDAGHYQWAATRGWNKFAGIFIGKUTGISIAWWKWTHNAHHIACNSLDY
DPDLQHLDMLAVSKLFNSITSVFYGROLTFDPLARFFVSYQHYLYYTHAWHIACNSLDY
LQTILLLISKRKIPDRGLNIGTLIFWTWFPLLVSRLPWPERVAFYLVSFCYTGIGH
LQTILLLISKRKIPDRGLNIGTLIFWTWFPLLVSRLPWPERVAFYLYGIGH
LQTILHFGGDVYVGPPRGDNWFEKQTRGTIDIACSSWMDWFFGGLOFOLHHFPRL
PRCHIKSISPICRELCKKYNLPYVSLSFYDANVTILKTLRTAALQARDLINFARQNEA
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                protein
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                                                                                                                                                                                                                                                             Length 1591;
            Indels
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Pred. No. 4.63e-240;
O; Mismatches 435;
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Pred. No. 4
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/codon_start=1
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Best Local Similarity 64.8%;
Matches 811; Conservative
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Sayanova,O., Smith,M.A., Shewry,P.R. and Napier,J.A.
Direct Submission
Submitted (20-NoV-1996) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS18 9AF, UK
Location/Qualifiers
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Pred. No. 1.78e-105;
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                                              754 GAGTCCTGAAATTCGACGAAGTGGCACGGTTCCTAGTCAGCTACCAGCACTGGACCTACT
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                                 1057 GAAAGCCTAAAGGGAATAATTGGTTTGAGAAACAAACGGATGGGACACTTGACATTCTT
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Pred. No. 2.20e-43;
229; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 7218)

Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.

Recombinant fowloox virus

Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers
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Sequence 14 from patent US 5670367.
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/product-"nitrate reductase"

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/translation="DDDKQFTMSEVRHGSKDSAWIVVHGHVYDCTGFLKDHPGGADS

/LIANGTDGTEEFDALHSDKAKALLDAHRIGELITTGAGYNSDNSVHAAP"

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Variation of nitrate reductase genes in selected grass species
Genome 38 (5), 919-927 (1995)
96076701
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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Liliopsida; Poales; Poaceae; Secale.
1 (bases 1 to 281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrate reductase.
Secale cereale DNA.
Secale cereale
Eukaryotae, mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALEKNRA 281 bp DNA PLN C
Secale cereale nitrate reductase gene, partial cds.
140154
9685205
                                                                                                                                                                                                                                                                                                                                                                                                      Length 965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                        Kitamura, K.
Ritamura, K.
Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 22;
Pred. No. 7.60e-12;
76; Mismatches 44
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Pred. No. 6.13e-10;
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    . 281
    /organism="Secale cereale"
    /db_xref="taxon:4550"

AR024229 965 bp DNA
Sequence 22 from patent US 5795961.
AR024229
93977523
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                                                                                                                                                                                                                                                                                                                       /organism="unknown"
170 c 226 g
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/codon_start=1
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1 Similarity 63.0%;
104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 17.4%;
Matches 26; Conservative
                                                                                                                             Unknown.
Unclassified.
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Matches 104; Conser
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                                                                                                         Unknown.
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/db_xref="PID:92305221"
/db_xref="PID:92305221"
/tb_mxravLidellavaQavSfadyvMeEWHTFKLEHRKNYQDET
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QLRAADESFKGYTFISPAHYTLEKSYDMRTKGAYTAYKDQGHGGSCWAFSSYGALEGG
HFRKSGYLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
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EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
ASSYPLV"
                                                                                                                                                                                   Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
                                                                                                                                                                                                                                                                                                                                                                      Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University
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Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, Universion
Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
                   GGCGCCGACAGCATCCTCATCAACGCCGGCACGGACTGCACCGAGGAGTTCGATGCCATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .10772
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
/gene="CP1"
                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                     05-AUG-1997
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/gene="CP1"
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                                                                  225
                                                                                     181 CACTCCGACAAGGCCCAAGGCGCTTCTCGACGCGCACCGCATCGGC
                                                                                                                                                                       NI
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Genetics 144 (4), 1601-1610 (1996)
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2310.
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6476. .6690
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/gene="CP1"
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872. .1000
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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AUTHORS
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REFERENCE
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/product="phenylalanyl trnA synthetase"
/db_xref="PiD:92305222"
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/db_yref="piD:9230522"
/db_yref="piD:923052"
/db_yref
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GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
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SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKOLFGPRIKYRWVDTYFPFTQPSWELEI
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Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
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                                                                                                                                                                                                                                                                                            /product="phenylalanyl tRNA synthetase"
join(8110. 9300,9370. >>9532)
/note="potential orf"
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Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualifiers
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Pred. No. 2.59e-09;
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Pred. No. 4.48e-08;
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                                                                                                                   6751. .7707
/gene="CP1"
                               6691. .6750
/gene="CP1"
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Local Similarity 19.0%;
Les 24; Conservative
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Best Local Similarity 18.3%;
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/db_xref="piD:g3305221"
/translation="MRTAVLPLLALLAVQANSFADVVMEEWHTFKLEHRKNYQDET
EERFRALSTENBRKHTARKHORPAEGKVSFKLAVNKYADLLHHEFRQLANGFNYTLHK
QLRAADESFKGVTFISPAHYILPKSVDWRTKGAVTAVKDQGHCGSCWAFSSTGALEGQ
HFRKSGVLYSLSEQNLVDCSTKYGNNGCNGGLANDARRYIKDNGGIDGSEKSYPAID
DSCHPRKGTVLPGOEBEKMABANATVGPVSVALDARSYPAID
DSCHPRKGTVALPGOEBEKMABANATVGPVSVALDARSTERFYFSEGYVA
EPOCDAQNLDHGVLVVGFGTDESGEDYMLVKNSWGTTWGDKGFIRMLRNKENOCGIAS
                                                                                                                                                                  AFUL2089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylajanyl tRNA synthetase gene, partial cds. 4F012089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 4553)
Gray, Y.H., Tanaka, M.M. and Sved, J.A.
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University, NSW 2006, Australia
738 AGGTGATGGAGTTGAAGAGTCGGGTGGAGACGCCGAATACGGGGATGTGCTGGAGGTCGG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gray, Y.H.M., Sved, J.Å., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
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join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
/gene="CP1"
                                                         896 RVITCRSSTIHGNGNIYYWYKGKAKYRVSNRSGVSRSGSGSGIDYIISSDAIYYC 950
                                                                                          Unpublished
(base 1 to 10772)
Gray, Y. H. M., Sved, J. A., Preston, C.R. and Engels, W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Science
**Current Processing**
**Control of Pro
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/gene="CP1"
/note="insertion site of P{CaSpeR}(50C)"
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/gene="CP1"
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6476. .6690
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
2310. .2426
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/product="phenylalanyl trna synthetase"
/db_xref="PID:92305222"
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PVYVYNONPMILIPADHVSRQKSDCYYINOQHLLRAHTAHQVELIGGGLDRFLVVG
EVYRNDEIDSTHYPVFHQADAVRLYKDKLFERNPGLEFEETWSGTLADPKLILPHP
                                                                                                                                                                                                                                                                                                            SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
YFKDWMLEWATULGGRINHELLQRSGYNGSIGYAFGVGLBRLAWTLEDIDPTRLFWBNDS
GFELSQPSEKDLHNLPRYKPFLSHYPQCTVDLSFWLPQDIEVDAGFSPNDFYDLYRSVAG
DWVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                           158 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 19; Length 107
Pred. No. 4.48e-08;
64; Mismatches 36; Indels
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Pred. No. 2.92e-06;
197; Mismatches 163; Indels
                                                                               /product="phenylalany1 tRNA synthetase"
join(8110. .9300,9370. .>9532)
/note="potential orf"
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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1491 c 1486 g
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6751. .7707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%;
Best Local Similarity 19.0%;
Matches 24; Conservative
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complement(10440. .11015)
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                                                                                                                                                                                                                                                                                                                              AC005369 74371 bp DNA PRI 01-AUG-1998
Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
1316 CAGCGTCCGAATTGTCCTGACATTAGCGTCCTCCCAAAACCCGGAAGCTCCTATACGGCAT 1257
                                            1136 CCACGGTGGGCACGTGATATCGATCGTCCTTTCGTCTGCTTCTCGAACCAGTTGTCGCC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 74371)
Klmmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Radner,K., Miguel,T., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.
Direct Submission
Submitted (01-ANG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
                                                                                                        Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7431)

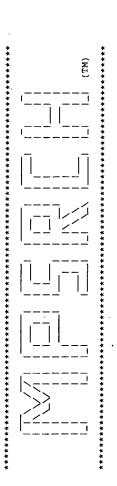
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Kadner, K., Miguet, T., Miller, C., Pitluck, S., Pollard, M., Sobramanian, S. and Martin, C.H.

Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished
                                                                           1256 CCCGTGCTTCTTACACAAGTCCCGAGCCAAGGGCGCAATCTTCCTAAGCTGCCCACGCGG
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Location/Qualifiers
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AC005369
g3367505
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KEYWORDS
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52388 .32488
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32617 .32617
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Db 15925 SKCSCMSRSKSKRGWGYRSWKKYRCAMWMTCKSSKCWCWSYRMRKCYSCSYCYCS-SGK 15983
                                                                                                                                                                                                                                                     15984 KYWCRCSMYWYICYYSYKYYWSMSYCICTSWGWRWMWSKGRSWMYASRSGCSCSCSMCMM 16043
                                                                                                                                                                                                                                                                                                                                    16044 CRCSCMSMKMWWTTTTTKTRTWTTTWKWRKAGASASRGKSKCRCMSYGKKSTCKMKMTC 16103
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                                                                                                                                        5;
                                                                                                  Length 74371;
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Best Local Similarity 13.3%; Pred. No. 7.36e-07;
Matches 28; Conservative 101; Mismatches 79; Indels
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                                                        annotations omitted
                                            Note: remainder of
                      misc_feature
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 244.06 Seconds 948.786 Million cell updates/sec Thu Feb 18 17:40:33 1999; Run on:

- n.a. database search, using Smith-Waterman algorithm

n.a.

MPsrch_nn

ular output not generated.

>US-08-934-254-26 tle:

(1-1702) from US08934254.seq 1702 Description: Perfect Score: N.A. Sequence:

.....TITITGGTAAAAAAAAA 1702

TABLE default Gap 6 Gap Scoring table:

Dbase 0; Query 0 •• STD Nmatch

188442 seqs, 68026449 bases x

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseg32 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part24 30:part30 31:part31 32:part32 33:part33 34:part34 40:part40

Mean 9.489; Variance 5.740; scale 1.653

istics:

1. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. Pred. No. score great and is der

SUMMARIES

Pred. No.	desatu 2.48e-94	d E.co 8.70e-13	_	_	٠.		sequence 1.47e-06	sequence 1.47e-06	sequence 1.47e-06	sequence 1.47e-06			
Description	Borage delta-6-desatu	Base substituted E.co	Oligonucleotide probe	Base substituted E.co	Oligonucleotide probe	Generic DNA sequence	Generic DNA sed	Generic DNA sed	Generic DNA sed	Generic DNA sed	DNA	DNA	
ΩI	T30395	N81164	051746	N81164	051746	070469	070468	070465	070470	070467	970472	070465	00.000
% Query Match Length DB	1685 21	204 1	91 9	204 1	91 9	114 12	114 12	114 12	114 12	114 12	114 12	114 12	
% Query Match	10.1	2.8	2.5	2.2	2.4	2.1	2.1	2.1	2.1	2.1	2.1	2.1	•
Score	172	47	43	43	40	36	36	36	36	36	32	36	,
Result No.	1	7	m	4	2	9	7	œ	σ	10	11	12	ŗ

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431 A;

1685 BP;

Seguence

1.47e-06 5.12e-06 1.77e-05 1.77e-05 2.02e-04	. 02e . 02e . 02e . 19e	.19e- .70e- .19e- .04e-		2.12e-01 2.12e-01 2.12e-01 2.12e-01 2.12e-01 2.12e-01
Generic DNA sequence Generic DNA sequence Generic DNA sequence Generic DNA sequence Generic DNA sequence	c DNA sequenc c DNA sequenc c DNA sequenc endothelin-1 interleukin 8 endothelin-1	ance P antisens erella alpina c nvelope region interleukin 8 se antisense ol	ixed oligonucl rimer used in eneric DNA seq eneric DNA seq uman vascular uman MDNCF ant ERI random pep treptomyces pr	Signal portion or gen Survival motor neuron Human survival motor Human survival motor Survival motor Survival motor Survival motor Survival motor neuron HSV-1 gB and surround Dictyostelium plasmid
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ALIGNMENTS

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Borage delta-6-desaturase gene.
Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
polyunsaturated fatty acid; octadecatetraeonic acid;
chilling resistance; oilseed; ss; ds.
Borago officinalis.
                                                                                                                                                                                                                                                                                                                                                                  Transgenic plants comprising the borage delta-6-desaturase geneshow increased production of gamma linolenic acid and having increased resistance to chilling claim 2; Page 51-52, 75pp; English.

A DNA clone (T30395) codes for borage delta-6-desaturase (R98455), which catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It was isolated from a borage membrane-bound polysomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library using probes based on abundantly expressed seed storage protein cDNAs and with an isolated partial cDNA clone. The gene can be incorporated into a vector, pref. incorporating a tissue-specific promoter, for the expression of delta-6-desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peant, carrot or oilseed rape, resulting in increased GLA prodn. Alteration of plant lipids may also lead to improved chilling resistance.
                                                                                                                                                                                                                                                                                                                 Thomas TL;
                                                                                                                                                                                                                                                                                         (RHON ) RHONE POULENC AGROCHIMIE.
Freyssinet GL, Nuccio M, Nunberg AN, Reddy AS,
                                                                                                                                                              Location/Qualifiers
T 1
T30395 standard; DNA; 1685 BP.
                                                    (first entry)
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30-DEC-1994; US-366779.
                                                                                                                                                                                                                                                                                                               Freyssinet GL, Nuc
WPI; 96-333997/33.
                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R98455
                                                      15-SEP-1996
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                                 T30395;
RESULT
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N81164;
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                                42 caatggotgotcaaatcaagaaatacattacotcagatgaaotcaagaaccacgataaac 101
                 Gaps
                                                                   ccggagatctatggatctcgattcaagggaaagcctatgatgtttcggattgggtgaaag
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Length 1685;
                 0; Mismatches 507; Indels
Score 172; DB 21;
Pred. No. 2.48e-94;
                 Conservative
        Best Local Similarity
Matches 697; Conser
Query Match
                                                                   102
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Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
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Random point mutations were introduced into the alpha fragment or E. coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can hamplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of wh.
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Base substituted E.coli beta galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escharichia coli.
LT 3
Q51746 standard; CDNA; 91 BP.
Q51746;
J-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988.
3-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen
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/function=multiple cloning site
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Pred. No. 8.70e-13;
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Sequence 204 BP; 21 A; 47 C: 17
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Local Similarity 12.8%;
les 15; Conservative
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624 IGGAAGIGGACCCACAACGCCCACACCTCGCATGCAACAGCCTCGACTACGACCCCGAC 683
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by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of Bandom point mutations were introduced into the alpha fragment of E. coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                     634 CCCACAAACGCCCACCACCACCACCTGGAACAGCCTCGACTACGACCGCGGACCTCAGC 690
                                                                                                                                                                                                MK14
but
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Base substituted E.coli beta galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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                                                                                                                                                                                             Oligonuclectide probe MK14.A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                    New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen
WPI; 88-279927/40.
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Pred. No. 1.79e-10;
.63; Mismatches 62; Indels
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187..204
/*tag= b
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Pred. No. 1.79e-10;
44; Mismatches 7
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                                                                                                                                                                                  Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N81164 standard; DNA; 204 BP
                                         01-DEC_1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                     2.5%;
Local Similarity 10.5%;
les 6; Conservative
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Best Local Similarity 17.8%;
Matches 27; Conservative
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/*tag= a
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30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                         Spears PA;
                                                                                                                    WPI; 93-378844/48
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                               EP-571911-A.
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Gaps

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                                   684 CICCAGCACATCCCCGTATTCGCCGTCTCCACCCGACTCTTCAACTCCATCACCTCGGTC 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Identifying proteins or peptide(s).which bind a ligand - by
screening a recombinant vector library expressing fusion proteins
comprising a binding domain and an effector domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1537 GGGAACGCAACCAGCTAGCAAAGTTAAGCAAAGTTAAGCTGAACGTAGTGCCTTC 1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide probe MK14'A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhv-vhhvhyhvyvsvctc
                                                                                                                                                                                                                                       31-Mar-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
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/note= "this sequence represents 'Z'; Z
sequence of 6,9 or 12 nucleotides (see
comments)"
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Pred. No. 9.00e-09;
47; Mismatches 4.
                                                                              154 ccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                   744 ITCTAIGGCCGAGICCIGAAAIICGACGAAGI
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Q70469 standard; DNA; 114 ВР
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Fowlkes DM, Kay BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp;
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/*tag=
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30-DEC-1993; US-176500
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26-MAY-1992; US-889651.
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This generic formula can be represented as follows: X(TCC)(NNB) 10-

(TCC)(NNB) 52 (NNB) 2(TCC)(NNB) 14 TCC) x and x are flanking restriction

sites (x is not the same as Y) that are not specified further. This

squence generates peptides that are cloverlast in structure. Other

generic sequences are shown in 070465-68. Other specific peptides

generic sequences are shown in 070465-68. Other specific peptides

concattenated by these generic sequences are shown in R6150-54. Tasks are

concattenated heterofunctional proteins or peptides, comprising at least

two functional regions - a binding domain with affinity for a ligand and

a second effector peptide portion that is chemically or biologically

cative They may further comprise a linker peptide between the 2 domains.

The oligonucleotides are also designed so that the expressed peptide

contains 2 or 4 cysteine residues positioned in, or flanking, the

conformational rigidity to the peptides. The TSARs or compsns. comprising

a TSAR binding domain can be used in vivo to deliver a chemically or
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                                                                                                                                                                                                                                                                                                                                                              a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
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Q70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)1(TGC) (NNB)2(2(NNB)7(TGC)(NNB)10Y: X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.
                       Q70469 is a generic DNA sequence used to generate random TSAR peptide
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Page 35; 255pp; English
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Sequence 114 BP; 0 A; 4 C
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01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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larity 5.5%;
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P-PSDB; R65154.
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Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affainty for a ligand and a second effector peptide portion that is chanically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs confers on compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. cell. They can also replace the function of macromolecules, eg. conduction. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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O70465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6/TGC)(NNB)112(NNB)14/TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specifies generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonuclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain broteins a generic base sold sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NN
in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the moleculary can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody activity allowing direct and rapid detection in a screening process. Sequence 114 BP, 0 A; 2 C; 2 G; 2 T;
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10-APR-1995 (first entry)
10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
ddirect; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 1
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Q70470 standard; DNA; 114 BP
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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3.6%;
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01-FEB-1994;
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

COMPACT is a generic DNA Sequence used to generate random TSAR (Totally Disclosure; Page 35; 255pp; English.

COMPACT is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) Peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)18; X

COMPACT SPECIFIC PEPTIDES (TAIS) FOR COMPACT (NNB)18; X

COMPACT SPECIFIC PEPTIDES GENERATE SEQUENCES are shown in R65151-54. TSARS are concatenated by these generic sequences are shown in R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the umpredicted or variant residues. Therefore residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the conformational antibodies and therefore circumvent the need for monoclonal or polyclonal antibodies and therefore circumvent the need for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
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                                                                                            3 bnnbnnbnnbcacnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnnnn 62
                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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    Length 114;
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  Score 36; DB 12; Length 114
Pred. No. 1.47e-06;
31; Mismatches 71; Indels
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/*tag= a
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/*tag= couperce of 6, 9 or 12 nucleotides (see comments)
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Pred. No. 1.47e-06;
34; Mismatches 74;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM. KAY BK;
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Q70467 standard; DNA; 114 BP.
    2.1%;
8.9%;
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Matches 4; Concer
Query Match
Best Local Similarity
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Q70468 standard; DNA; 114 BP.
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Similarity 4.7%;
5; Conservative
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain

PI comprising a binding domain and an effector domain

Disclosure; Page 36; 255pp; English.

CQ70472 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)!(CAC)(NNB)!(CAC)(NNB)!CAC)(NNB) (CAC)(NNB) (CAC) (NNB) (
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
                                                                                                                                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                         GGGCAAGGTCTACGACTGCTCTCGGTGGGCGGGGGAGCACCCCGGCGGCGAG 182
                                   CITGCIGIGGATCCAAGCCGCGTAIGIGGGCCATGACTCCGGCCATTAC 542
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Pred. No. 5.12e-06;
28; Mismatches 69; Indels
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31-JAN-1994; US-189331.
(UXNC.) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
WPI: 94-279739/34.
P-PSDB: R58383.
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Best Local Similarity 11.0%;
Matches 12; Conservative
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Q70472 standard; DNA; 114
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01-FEB-1994;
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10-APR-1995
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Person and Rolls.

Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

Py Screening a recombinant vector library expressing fusion proteins

Py Screening a recombinant vector library expressing fusion proteins

Disclosure: Page 35; 255pp; English.

Disclosure: Page 35; 255pp; English.

CC (70465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides: This generic formula can also be represented as follows: X(NNB)6(CGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are constrainty further. Other specified further. Other specified further. Other specified further. Other specified proteins or peptides.

CC offer specified further. Other furtional regions - a binding domain with a first two functional regions - a binding domain with a first two functional regions - a binding domain with a first two functional regions - a binding domain with a first the expressed peptide contains 2 or 4 cysteine residues positioned in or flanking, the unpredicted or variant residues positioned in or flanking, the unpredicted or variant residues positioned in or compass. Comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, calliver a chemically or biologically active moiety, eg. metal ion, conformation or polyclonal antibodies and therefore circumvent the need for computer methods of hybridoma formation or in vivo antibody conformation. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 C; 2 C; 2 C;
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effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents '2'; 2 can be
                                                                                                                                                                                                                                                                                                        can
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Pred. No. 1.47e-06;
32; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                    /note= "this sequence represents 'Z'; Z sequence of 6, 9 or 12 nucleotides (see comments)"
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                                                                                                                                          Location/Qualifiers
55..60
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유 ò 윱 à

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30-DEC-1993; US-176500
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Best Local Similarity
                                                                                                 WPI; 94-279739/
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                                                                                                                                      P-PSDB; R65153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discussure; Ages 23; Aspep; Lenglish.

Off 468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be copresented as follows: X(NNB)1(TGC)(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68.

Other specified further other generic sequences are shown in R65151-54. TSARs are concatenated beterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a f65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a f65151-64. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functions. They may further comprise a linker of peptide between the 2 domains. The Oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the umpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, cadioisotope, peptide, toxin or enzyme, to the specific target or on the conclusion or prolyclonal antibodies and therefore circumvent the need for complex methods of hybridoma deterior or in vivo antibody conclusions of hybridoma deterior or in vivo antibody activity and allowing direct and rapid detection in a screening process.

Secuence 114 RP: 0 A Discounted and a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 GCAGGCGAGGTGGGCGTTGTGGGTCCACCACCACCACGATGCTGATTCCGGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure, Page 35, 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / cd | Lhis sequence represents 'Z'; Z can be sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     599 GAIGTIGCCIGCTATGAGTIGCGTGTATCTATCCACGGGTTGGCATC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanb 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.47e-06;
33; Mismatches 74; Indels
   or 12 nucleotides (see
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G;
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sequence of comments)"
                                                                                                                                                                                                                          31-Jan-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
WPI: 94-27939/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 4.5%;
5; Conservative
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US-176500.
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                                                                                                                                                          01-FEB-1993; US-013416
30-DEC-1993; US-176500
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Best Local Similarity
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01-FEB-1994; (01-FEB-1993; (30-DEC-1993; (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); (1993); 
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Tdentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins per screening a recombinant vector library expressing fusion proteins per comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

CY0467 is a generic DNA sequence used to generate random TSAR (Totally Disclosure, Page 35; 255pp; English.

CY0467 is a generic DNA sequence used to generate random TSAR (Totally CY0467 is a generic DNA Sequence used to generate of an also be represented as follows: X(NNB)5[GTGC)(NNB)12(NNB)16(TGC)(NNB)17. X and Y are flanking restriction sites (X is not the same as Y) that are controlled further. Other generic sequences are shown in CASISI-34. TSARS are concatenated by these generic sequences are shown in R65151-34. TSARS are concatenated by these generic sequences are shown in CASISI-34. TSARS are concatenated by these generic sequences are shown in Affinity for a ligand and a second effector peptide protein with a affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed to that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ior on the complex methods of hybridoma formation of macromolecules, eg.

Cell. They can also replace the function of macromolecules, eg.

Cell. They can also replace the function of macromolecules, eg.

Cell. They can also replace the function of macromolecules, eg.
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/note= "this sequence represents 'Z'; Z can
sequence of 6,9 or 12 nucleotides (see
comments)"
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Pred. No. 1.47e-06;
33; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         direct and rapid detection in a screening process. Sequence 114 BP: 0 A; 2 C; 2 G; 2 T;
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Q70469 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK;
(UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%;
Similarity 2.8%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-1995 (first entry)
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This generic formula can be represented as follows: X(TGC)(NNB)10-
CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
cstemences are shown in Q70465-68. Other specific peptides
Generated by these generic sequences are shown in R65150-54. TSARS are
concatenated heterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
contains 2 or 4 cysteine residues positioned in, or flanking, the
contains 2 or 4 cysteine residues positioned in, or flanking, the
conformational rigidity to the peptides. The TSARs or comprising
cumpredicted or variant residues positioned in, or flanking, the
conformational rigidity to the peptides. The TSARs or comprising
conformational rigidity to the peptides. The TSARs or comprising
conformational rigidity to the peptides. The TSARs or comprising
conformational rigidity to the peptides. The TSARs or comprising
conformation of macromolecules, eg. monoclonal or polyclonal antibodies
and therefore circumvent the need for complex methods of hybridoma
conformation or in vivo antibody production. The TSARs are easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 G;
Disclosure; Page 35; 255pp; English.
Q70469 is a generic DNA sequence use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n a screening process.
114 BP; 0 A; 4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection in
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Gaps ö Score 35; DB 12; Length 114; Pred. No. 5.12e-06; 31; Mismatches 71; Indels 2.1%; llarity 6.4%; Conservative Query Match
Best Local Similarity
Matches 7; Conser

6 banbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbannban

d Cp g

1067 GCCCACGTATGTGTCGCCGGAGAAGTGGTTGAGCGTGAACTGGACGTGC 1019 Cp

Search completed: Thu Feb 18 17:49:40 1999 Job time : 547 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein . protein database search, using Smith-Waterman algorithm Thu Feb 18 11:36:06 1999; MasPar time 13.22 Seconds 917.710 Million cell updates/sec

Lar output not generated.

>US-08-934-254-27 (1-452) from USO8934254.pep 3515 1 MEGEAKKYITAEDLRRHNKS......LNSAPCPKKLGYGEAYNTHG 452 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

74019 segs, 26840295 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

swiss-prot35 1:swissprot Database:

Mean 51.005; Variance 92.089; scale 0.554 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No	3.17e-2		1.15e-1	2.72e-1	۲.	3.51e-1	4.45e-1	4.45e-1	4.45e-1	1.91e-1	6.78e-1	•	6.78e-1	2.39e-1	8.35e-1	2.90e-1	1.27e-1	1.27e-1	1.92e-1	2.90e-1	2.90e-1	4.39e-1	9
	,	REDU	1 (E	1 (E	CLO	CLO) E	2 (E	2 (E) E) EC) 일	(NAD		SIC	REDU	1 (E	2 (E) E	(NAD	OUTER M
	Description	INDUCIBLE NITRATE	NITRATE REDUCTASE	NITRATE REDUCTASE	NITRATE REDUCTASE,	NITRATE REDUCTASE,	CYTOCHROME B5.	CYTOCHROME B5.	CYTOCHROME B5.	NITRATE REDUCTASE	CYTOCHROME B5.	CYTOCHROME B5, SEED	INDUCIBLE NITRATE	NITRATE REDUCTASE	NITRATE REDUCTASE	NITRATE REDUCTASE	NITRATE REDUCTASE	CYTOCHROME B5, OUT						
	DI	NIA2_SOYBN	NIA1_PHAVU	NIA1_ARATH	NIA1_BRANA	NIA2_BRANA	CYB5_TOBAC	CYB5_YEAST	CYB5_ORYSA	NIA_LOTJA	NIA2_ARATH	NIA2_PHAVU	NIA_LYCES	NIA_CUCMA	NIA_SPIOL	NIA_BETVE	CYB5_BRAOL	CYS5_TOBAC	NIA1_SOYBN	NIA1_TOBAC	NIA2_TOBAC	NIA_PETHY	NIA_NEUCR	CYM5_RAT
	DB	н	Н		Н	Н	٦	7	Н	Н	П	Н	Н	Н	Н	Н	Н	 (1	Н	Н	Н	Н	Н
	Query Match Length	890	881	917	911	911	136	120	137	900	917	890	911	918	926	868	134	135	886	904	904	606	982	92
æ	Query	6.3	6.2	6.2	6.1	0.9	5.9	5.8		5.8		5.7	5.7	5.7	5.7	٠.	5.5	-:	-:	5.5	-:		5.5	5.4
	Score	220	219	217	215	212	209	203	203	203	202	202	200	202	199	196	193	195	195	194	193	193	192	191
	Result		7	m	4	Ŋ	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.51e-14	5.19e-14	5.19e-14	2.65e-13	1.76e-13	2.65e-13	6.65e-12	2.98e-12	2.19e-11	2.19e-11	3.26e-11	3.26e-11	3.26e-11	1.07e-10	7.19e-11	1.58e-10	1.58e-10	2.33e-10	3.45e-10	5.09e-10	5.09e-10	5.09e-10
NITRATE REDUCTASE (NAD	NITRATE REDUCTASE (EC	NITRATE REDUCTASE (EC	NITRATE REDUCTASE (EC	NITRATE REDUCTASE 1 (E	NITRATE REDUCTASE (EC	NITRATE REDUCTASE 3 (E	NITRATE REDUCTASE (NAD	CYTOCHROME B5.	CYTOCHROME B5.	CYTOCHROME B5 (FRAGMEN	CYTOCHROME B5.	CYTOCHROME B5.	CYTOCHROME B5.	HYPOTHETICAL 16.7 KD P	CYTOCHROME B5 (CYTB5).	CYTOCHROME B5.	CYTOCHROME B2 PRECURSO	NITRATE REDUCTASE (EC	CYTOCHROME B5.	CYTOCHROME B5.	CYTOCHROME B5.
NIA7_HORVU	NIA2_HORVU	NIA1_HORVU	NIA1_MAIZE	NIA1_ORYSA	NIA_CICIN	NIA3_MAIZE	NIA_FUSOX	CYB5_HORSE	CYB5_RABIT	CYB5_ALOSE	CYB5_HUMAN	CYB5_PIG	CYB5_BOVIN	YDAA_SCHPO	CYB5_MUSDO	CYB5_CHICK	CYB2_HANAN	NIA_VOLCA	CYB5_RAT	CYB5_MOUSE	CYB5_CUSRE
-	Н	Н	Н	П	٦	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	ч	-1	-	Н		-
891	912	915	621	916	920	889	902	133	133	87	133	133	133	147	134	138	573	864	133	133	135
5.4	5.3	5.3	5.2	5.2	5.2	5.0	5.0	•	4.9	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.6	4.6	4.6
189	186	186	182	183	182	174	176	171	171	170	170	170	167	168	166	166	165	164	163	163	163
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

513 MNTISKIYIMSE-VRRHNNADSAWIIVHGHVYDCIRFLKDHPGGIDSILINAGTDCIEEF 571

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Score 220; DB 1; Length 890; Pred. No. 3.17e-20; 16; Mismatches 26; Indels 1; Gaps

Query Match 6.3%; Best Local Similarity 41.1%; Matches 30; Conservative

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ద à RESULT ID NI DT 01 DT 01 DT 01 DT 01 OC 01 EN NI CO EER NI EER

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SEQUENCE FROM N.A. .
STRAIN=CV. LISANDRA;
MEDLINE; 96222419.
FUKUOKA H., OGAMA T., MINAMI H., YANO H., OHKAWA Y.;
FUKUOKA H., OGAMA T., MINAMI H., YANO H., OHKAWA Y.;
PLANT PHYSIOL. 111:39-47(1996).
-i- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.TERMINAL DOMAIN.
-!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C.TERMINAL DOWNIN.
-- EMBL; X13436, G22757; --
-- EMBL; X13436, G295791; --
-- EMBL; X13436, G295791; --
-- PIR; S35228; S35228.
-- PIR; S35228; S35228.
-- PIR; S32018; S32018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 MNTASKMYSISE-VRKHNTADSAWIIVHGHIYDCTRFLKDHPGGTDSILINAGTDCTEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRASSICA NAPUS (RAPE).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 217; DB 1; Length 917;
Pred. No. 1.15e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P17571; ZCND.
PROSITE; PS00191; CYTOCHROME_B5; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE; FLAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE, CLONE PBNPR1405 (EC 1.6.6.1) (NR).
                                                                         [2]
SEQUENCE OF 342-360 AND 525-917 FROM N.A.
MEDLINE; 89091069.
                     WILKINSON J.Q., CRAWFORD N.M.;
MOL. GEN. GENET. 239:289-297(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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93287999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
NIA1_BRANA
P39867:
  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-CV. SAXA; TISSUE-SHOOT;

HOFF T., STUMANN B.M., HENNINGSEN K.W.;

HOFF T., STUMANN B.M., HENNINGSEN K.W.;

HYSIOL. FLANTARUM 8.M., HENNINGSEN K.W.;

PHYSIOL. FLANTARUM 8.M., HENNINGSEN K.W.;

C.!- FUNCTION: NITRATE ASSIMILATION IN PLANTS, FUNGE AND BACTERIA.

STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGE AND BACTERIA.

C.!- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

C.!- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

C.!- SUBUNIT: HOMODIMER (BY SIMILARITY).

C.!- SIMILARITY: TO EUKRYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE

N.TERMINAL DOMAIN.

C.!- SIMILARITY: TO FAB/NAD-BINDING CYTOCHROME REDUCTASES IN THE

C.!- SIMILARITY: TO FAB/NAD-BINDING CYTOCHROME REDUCTASES IN THE

C.!- SIMILARITY: TO FAB/NAD-BINDING CYTOCHROME REDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE 1 (EC 1.6.6.1) (NR-1).
NIAL OR NR.
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 MNTATKSY-SLSEVRRHNNRDSAWIIVNGHVYDCTRFLKDHPGGEDSILLNAGTDCTEEF 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEGEAKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGODVTDAF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: ...
-!- SIMILARITY: ...
C-TERMINAL DOMAIN.
JR EMBL, X53603; G21019; ...
DR PROSITE: PS00191; CYTOCHROME B5; 1.
DR PROSITE: PS00199; MOLYBDOPTERIN_EUK; 1.
DR PROSITE: PS00199; MOLYBDENUM; PROSITE PROSITE: PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 219; DB 1; Length 881;
Pred. No. 4.87e-20;
15; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPDATE)
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                                                                                                                                                                        881 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.T. 3

NIAL_ARATH STANDARD; PRT; 917 AA P11832;
01-0CT-1989 (REL. 12, CREATED)
01-UNN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE 1 (EC 1.6.6.1) (NR1).
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 6.2%;
Local Similarity 41.1%;
les 30; Conservative
                                                                                                                                                                          STANDARD;
                     572 EAIHSDKAKQMLE 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                570 EAIHSDKAKKMLE 582
                                                    | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                LT 2
NIA1_PHAVU
P39865;
                                                                                                                                                                                                                                                                                                                                                                                                            FABACEAE.
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TRANSMEM
CONFLICT
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STRAIN-CV. LISANDRA;

WEDLINE; 96222419.

PLANT PHYSIOL. 111:39-47(1996).

-!-FUNCTION: NITRAITE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST STEP OF NITRAITE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

-!-CAPALYIC ACTIVITY: NADH + NITRAITE = NAD(+) + NITRITE + H(2)O.

-!-COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

AND ONE MOLYBDENUM ATOM.

-!-SUBUNIT: HOMODIMER (BY SIMILARITY).

-!-SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                     -!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C-TERMINAL DOMAIN.
EMBL; D38219; 6540465; -.
PROSITE; PS00191; CYTOCHROME B5; 1.
PROSITE; PS00191; CYTOCHROME B5; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE; FLAVOPROTEN: FAD): NAD; HEME; MOLYBDENUM;
NITRATE ASSIMILATION; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535 MNTASKMYSMSE-VRKHNSAESAWIIVHGHIYDCTRFLKDHPGGSDSILINAGTDCTEEF 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C-TERMINAL DOMAIN.
                                              AND ONE MOLYBDENUM ATOM.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
    CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O. COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TERMINAL LOLL.

EMBL; D38220; G540487; --

R PROSITE; PS00191; CYTOCHROME_B5; 1.

R PROSITE; PS00191; CYTOCHROME_B5; 1.

W OXIDOREDUCTASE; FLAVOPROTEIN, FAD; NAD; HEME; MOLYBDENUM;

W NITRATE ASSIMILATION; MULTIGENE FAMILY.

FT METAL 191 MOLYBDENUM-PIERIN (POTENTIAL).

FT METAL 245 MOLYBDENUM-PIERIN (POTENTIAL).

FT DISULFID 430 430 INTERCHAIN (POTENTIAL).

FT BINDING 574 574 HEME LIGAND (BY SIMILARITY).

FT BINDING 597 597 HEME LIGAND (BY SIMILARITY).

FT BINDING 597 597 HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                    MOLYBDENUM-PTERIN (POTENTIAL). MOLYBDENUM-PTERIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
                                                                                                                                                                                                                                                                                                                                                                                  130 INTERCHAIN (POTENTIAL).
574 HEME LIGAND (BY SIMILARITY).
102252 MW; 57A3E33B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (REL. 31, CREAȚED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CTT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE, CLONE PBNBR1412 (EC 1.6.6.1) (NR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 215; DB 1; I
Pred. No. 2.72e-19;
18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.1%;
Local Similarity 38.4%;
Les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAPPARALES; CRUCIFERAE.
                                                                                                                    N-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRASSICA NAPUS (RAPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 EAIHSDKAKKLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIA2_BRANA
P39868;
01-FEB-1995 (
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ry Match
                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SET TET TET SO
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AMILIARY A.S. STOBART A.K., SHEWRY P.R., NAPIER J.A.;
MIDLIARE; 94.294/0.

21. FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND
OXYGENASES. MAY PLAY A REY ROLE IN THE MODIFICATION BY
DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
THE DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
ANY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS AND IN THE PETALS.
C.I. SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
C.I. TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
MODIFICATION SIDE OF THE LEAF.
CYTOPLASMIC SIDE OF THE LEAF.
C.I. TISSUE SPECIFICITY: IS HIGHLY EXPRESSED AT LOW
LEVELS IN THE LEAF.
C.I. TISSUE SPECIFICITY: THANSWERE ALT.INIT.
C.I. TISSUE SPECIFICITY: THANSWEREARS, HEME; MICROSOME; MULTIGENE FAMILY.
EMBL; X68140; G19853; -
EMBL; X68140; G19853; -
EMBL; X68140; G19853; -
EMBL; X68140; G19853; -
EMBL; X68140; G19854; ALT.INIT.
EMBL; MANSPORT; TRANSMEMBRARE; HEME; MICROSOME; MULTIGENE FAMILY.
EMBL; MANSPORT; TRANSMEMBRARE; HEME; MICROSOME; MULTIGENE FAMILY.
EMBL; MANSPORT; TRANSMEMBRARE;
EMBL;
EM
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                                                                                                                                         535 MNTSAKMYSMSE-VRKHNSVESAWIIVHGHIYDCTRFLKDHPGGSDSILINAGTDCTEEF 593
                                                                                                                                                                                     1 MGGETKVFTLAE-VSQHNNAKDCWLVISGKVYDVTKFLDDHPGGDEVLLSATGKDATDDF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                            Gaps
                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 136;
   Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Indels
                                                                        27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LA -> EF (IN G19853).
MISSING (IN G19853).
6F34BDD9 CRC32;
   Score 212; DB 1; 1
Pred. No. 9.79e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 209; DB 1; Pred. No. 3.51e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
CYTOCHROME B5.
                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NICOTIANA TABACUM (COMMON TOBACCO)
EUKARYOTA; PLANTA; EMBRYOPHYTA; AN
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 31, CREATED)
(REL. 34, LAST SEQI
(REL. 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14979 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 EDVGHSSSARAMLDEYYVG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IAY-HPGTAWRHLDPLFTG 78
Query Match 6.0%;
Best Local Similarity 39.7%;
Matches 29; Conservative
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Best Local Similarity 41.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                   594 EAIHSDKAKKLLE 606
                                                                                                                                                                                                                                                                                                                              | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=LEAF;
MEDLINE; 94325476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYB5_YEAST
P40312;
01-FEB-1995 (
01-OCT-1996 (
01-NOV-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 6
CYB5_TOBAC
P49098;
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                  Matches
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SO FTT SO
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                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97245296.

DE ANTONI A., D ANGELO M., DAL PERO F., SARTORELLO F., PANDOLFO D., PALLAVOTINI A., LANFRANCHI G., VALLE G.;

PALLAVICINI A., LANFRANCHI G., VALLE G.;

TEAST 13:261-2661997).

-:- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SYFERAL MEMBRANE BOUND OXYGENASES. IT PLEXS A ROLE IN FATTA-ACID DESATORATION AND IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PKVY-SYQEVAEHNGPENFWIIIDDKVYDVSQFKDEHPGGDEIIMDLGGQDATESFVDIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | : ::: || : ::|| |: |||| |: ||||||| ::|:
5 AKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAY- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INMOSTEROL.

SUMOSTEROL.

CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

EMBL; L22494; G431762; -.

EMBL; Z69382; E221832; -.

EMBL; Z73387; E229931; -.

EMBL; Z71387; E229931; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITH M.A., STOBART A.K., SHEWRY P.R., NAPIER J.A.;
PLANT MOL. BIOL. 25:527-537(1994).
-!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXYGENASES.
-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE_OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CYTOCHROME B5.
ORYZA SATIVA (RICE)
CURRARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
CYPERALES; GRAMINEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                              MEDLINE; 94237477.
TRUAN G., EPINAT J.-C., ROUGEULLE.C., CULLIN C., POMPON D.;
GENE 142:123-127(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 6.1.2.

PIR; 847919; 847919.

SGD; 1000249; CXB5.

PROSITE; PS0101; CYTOCHROME_B5; 1.

ELECTRON TRANSPORT; TRANSMEMBRANE; HEME; MICROSOME.

**TANSMEMBRANE; HEME LIGAND (BY SIMILARITY).

**ANTAL.**

**ANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 203; DB 1; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.45e-17;
19; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
E -> Q (IN REF. 1).
9BEA894F CRC32;
                      CYBS OR YNL111C OR N1949.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMBL; X75670; G414705; -.
PROSITE; PS00191; CYTOCHROME_B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13297 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.8%;
Best Local Similarity, 38.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HSDEALRLLKGLYIG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPGTAWRHLDPLFTG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
98
17
120 AA;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 97245296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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CYTOCHROME B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=CALLUS
                                                                                                                                                                                    STRAIN-FL100
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P49100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
CONFLICT
SEQUENCE
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CCC RARRERES CCC RARRES CCC RARRES CCC CCC RARRES CCC CCC RARRES CCC CCC RARRES CCC R
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO GIFU / B-129;

A WATERHOUSE R.N., SMTH A.J., PROSSER I.M., FORDE B.G., CLARKSON D.T.;

SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

-!- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

C -!- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

C -!- SUBMITT: HOWODIMER (BY SIMILARITY).

C -!- SIMILARITY: TO EUGRARYOTIC MOLYBDOPPERIN OXIDOREDUCTASES IN THE

N-TERMINAL DOMAIN.

C -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE

C -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOTUS JAPONICUS.
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 MNTFTKMY-SLSEVKKHNSPDSAWIIVHGHVYDCTRFLKDHPGGADSILINAGTDCTEEF 575
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                  1 MSNDNKKVYTLEEVAKHNSKDDCWLIIGGKVYNVSKFLEDHPGGDDVLLSSTGKDATDDF
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226 MOLYBDENUM-PTERIN (POTENTIAL).
411 INTERCHAIN (POTENTIAL).
556 HEME LIGAND (BY SIMILARITY).
101420 MW; 2F667418 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 203; DB 1; Length 900;
Pred. No. 4.45e-17;
19; Mismatches 26; Indels
                                                                                                                                                               Length 137;
ELECTRON TRANSPORT; TRANSMEMBRANE; HEME; MICROSOME.

BINDING 41 41 HEME LIGAND (BY SIMILARITY).

65 65 HEME LIGAND (BY SIMILARITY).

TRANSMEM 108 128 POTENTIAL.

SEQUENCE 137 AA; 15296 MW; B204EA8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X80670; G517356; -.
PIR; S47029; S47029.
PROSITE; PS00191; CYTOCHROME_B5; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
OXIDORBOUCTARE; FLAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM; NITRATE ASSIMILATION.
                                                                                                                                                            Score 203; DB 1; Length 137
Pred. No. 4.45e-17;
13; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
1-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE (EC. 1.6.6.1) (NR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              | ||: :| :|
61 IAY-HPGTAWRHLDPLFTG 78
                                                                                                                                                                                                                                                                                                                                                                             61 EDVGHTTTARAMMDEYYVG 79
                                                                                                                                                               Query Match 5.8%;
Best Local Similarity 40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%;
Best Local Similarity 37.0%;
Matches 27; Conservative
                                                                                                                                                                                                                   32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 EAIHSDKAKKMLE 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : | : |:
IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    900 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL.
01-FEB-1995 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
NIA_LOTJA
P39869;
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917 AA

PRT;

STANDARD;

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-!- CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.
-! COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
-! ERME IRON, AND MOLYBDENINH-PTERIN AS PROSTHETIC GROUPS. THE HEME
GROUP IS CALLED CYTOCHROME B-557.
-! SUBUNIT: HOMODIMER.
-! TISSUE SPECIFICITY: ROOT, LEAR, AND SHOOT.
-! WHEN MUTATED CONFERS RESISTANCE TO THE HERBICIDE CHLORATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 MNTTAKMYSMSE-VKKHNSADSCWIIVHGHIYDCTRFLMDHPGGSDSILINAGTDCTEEF 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93287999.
WILKINSON J.Q., CRAWFORD N.M.;
MOL. GEN. GENET, 239:289-297(1993).
-i- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEMB-BINDING DOMAIN.
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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HSEP; PI7571; 2CMC.
HSEP; PI7571; 2CMC.
PROSITE; PSO0191; CYTOCHROME_B5; 1.
PROSITE; PSO0559; MOLYBDEPTERIN_EUK; 1.
PROSITE; PSO0559; MOLYBDEPTERIN_EUK; 1.
PROSITE; PSO0559; MOLYBDENUM; PADI, HEME; MOLYBDENUM;
NITRATE ASSIMILATION; MULTIGENE FAMILY; HERBICIDE RESISTANCE.
METAL 191 MOLYBDENUM-PTERIN (POTENTIAL).
245 MOLYBDENUM-PTERIN (POTENTIAL).
                                                                                                                                                                                                                                                      EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHENG C., DEWDNEY J., NAM H., DEN BOER B.G.W., GOODMAN H.M.;
EMBO J. 7:3309-3314(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 205; DB 1; Length 917;
Pred. No. 1.91e-17;
18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (POTENTIAL).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
7; 95608AFB CRC32;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CY. COLUMBIA;
MEDLINE; 88278888.
CRAMFOND N.M., SMITH M., BELLISSIMO D., DAVIS R.W.;
PROC. NATL. ACAD. SCI. U.S.A. 85:5006-5010(1988).
                                                    01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NITRAPE REDUCTASE 2 (EC 1.6.6.1) (NR2).
NARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J03240; G166782; -.
EMBL; X13435; G930002; -.
EMBL; S45385; -; NOT_ANNOTATED_CDS.
PIR; A31821; RDMUNH.
PIR; S01641; S01641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93005711.
WILKINSON J.Q., CRAWFORD N.M.;
PLANT CELL 3:461-471(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 522-917 FROM N.A. MEDLINE; 89091069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%;
Best Local Similarity 38.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A.
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433
577
600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERBICIDE RESISTANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   917 AA;
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SEQUENCE
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                                                                                                                                      PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DANIEL-VEDELE F., DORBE M.F., CABOCHE M., ROUZE P.;
GENE 85:371-380(1989).
-!- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 MNTASKMF-SVSEVKKHSSPDSAWIIVHGHVYDCTRFLKDHPGGTDSILINAGTDCTEEF 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYCOPERSICON ESCULENTUM (TOMATO).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTRATE ASSIMILATION: MULTIGENE FAMILY.

METAL. 165 165 MOLYBDENUM-PTERIN (POTENTIAL).

METAL. 219 219 MOLYBDENUM-PPERIN (POTENTIAL).

BISULEN 548 140 HEME LICAND (BY SIMILARITY).

BINDING 571 571 HEME LICAND (BY SIMILARITY).

SECUENCE 890 AA; 99995 MW; D952FE9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U01029; G392992; -.
PROSITE; PS00191; CYTOCHROME_B5; 1.
PROSITE: PS00595; MOLYBOOPTERIN_ENK; 1.
OXIDOREDUCTASE; FLAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 202; DB 1;
Pred. No. 6.78e-17;
                                                                 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AGG-1990 (REL. 15, CREATED)
01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE (EC 1.6.6.1) (NR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA
                 890 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. MANAPAL; TISSUE-LEAF;
MEDLINE; 90185211.
                                                   01-FEB-1995 (REL. 31, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 5.7%;
Local Similarity 34.2%;
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 DAIHSDKAKKMLE 580
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                                                                                                                        NIA2 OR NR2.
LT 11
NIA2_PHAVU
P39866;
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NIA_LYCES
P17570;
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MEDLINE; 92084635.
HYDE G.E., CRAWFORD N.M., CAMPBELL W.H.;
J. BIOL. CHEM. 266:23542-23547(1991).
-!- FUNCTION: NITRATE REDUCTASE IS A KEY ENIYME INVOLVED IN THE FIRST
STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
-!- CATALXITI ANDH + NITRATE = NAD(+) + NITRITE + H(2)O.
-!- COFACTOR: EACH SUBUNIT OF THE ENIYME CONTAINS I EQUIVALENT OF FAD,
HEME IRON, AND MOLYBDENUM PETERIN AS PROSTHETIC GROUPS. THE HEME
GROUP IS CALLED CYTOCHROME B-557.
                                                                                                                                                                                                                                                                                                                            532 MNTASKMYSMSE-VRKHNSSDSAWIIVHGHIYDASRFLKDHPGGVDSILINAGTDCTEEF 590
                                 -!- SUBUNIT: HOMODIMER.
-!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
N-TERMINAL DOMAIN.
-!- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-:- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
EMBL; M33154; G167499; -
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- INDUCTION: BY NITRATE.
-!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
N-TERMINAL DOMAIN.
CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O. COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557) AND ONE MOLYBDENUM ATOM.
                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-UUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE (EC. 1.6.6.1) (NR)
CUCUBBITA MAXIMA (PUMPKIN) (WINTER SQUASH).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                         MOLYBDENUM-PTERIN (POTENTIAL).
MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
HEME LIGAND (BY SIMILARITY).
HENE LIGAND (BY SIMILARITY).
HENE LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                             Score 200; DB 1; Length 911;
Pred. No. 1.57e-16;
16; Mismatches 27; Indels
                                                                                                      EMBL; X14066; G19283; -.
PIR; JQ0373; RDTONH.
HSSP; P17571; 2CND.
PROSITE; PS00191; VATOCHROME_B5; 1.
PROSITE; PS0559; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE; FLAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRAWFORD N.M., CAMPBELL W.H., DAVIS R.;
PROC. NATL. ACAD. SCI. U.S.A. 83:8073-8076(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  918 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A41667; A41667.
HSSP; P17571; 2CND.
PROSITE; PS00191; CYTOCHROME_B5; 1.
                                                                                                                                                                                                                                                      102453 MW;
                                                                                                                                                                                                                                                                            Query Match 5.7%;
Best Local Similarity 39.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           591 DAIHSDRAKKLLE 603
                                                                                                                                                                                                                                                                                                                                                                                        | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                                                 LATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                 NITRATE ASSIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 13
NIA_CUCMA
P17569;
                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                           BINDING
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SHIRAISHI N., KUBO Y., TAKEBA K., KIYOTA S., SAKANO K., NAKAGAWA H.; PLANT CELL PHYSIOL. 32:1031-1038(1991).
-!- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
-!- CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.
-!- COPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS I EQUIVALENT OF FAD.
HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:-SIMILARITY: CONTAIN.
-:-SIMILARITY: CONTAIN.
-:-SIMILARITY: CONTAIN.
-:-SIMILARITY: CONTAIN.
-:-SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE CTERMIRAL DOWAIN.
EMBL: M32600; G170119; -.
EMBL: D86226; D1013734; --
EMBL: U08029; G470678; -.
PIR: S11868; RDSPNH.
HSSP: P17571; ZCND.
PROSITE: PS00191; CYTOCHROME_B5; 1.
PROSITE: PS00191; CYTOCHROME_B5; 1.
PROSITE: PS0059; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE: ELAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                                                                                                                                       539 MNTASNTY-TLSEVKKHNSPQSAWIIVHGHVYDCTRFLKDHPGGSDSILINAGTDCTEEF 597
                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROUP IS CALLED CYTOCHROME B-557.
-!- SUBMIT: HOMODIMER.
-!- SIMILARIT: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPINACIA OLERACEA (SPINACH).
EURARXOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLYBDENUM-PTERIN (POTENTIAL). MOLYBDENUM-PTERIN (POTENTIAL).
                                                                                                         MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                           DB 1; Length 918;
                                                                                  MOLYBDENUM-PTERIN (POTENTIAL)
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE; FLAVOPROTEIN; FAD; NAD; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                           Score 202; DB 1; Length 918
Pred. No. 6.78e-17;
18; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE; 97273959.
TAMURA N., TAKAHASHI H., TAKEBA G., SATOI T., NAKAGAWA
BIOCHIM. BIOPHYS. ACTA 1338:151-155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIA_SPIOL STANDARD; PRT; P23312; Q41377; 01-NOY-1991 (REL. 20, LAST SEQUENCE U 15-UTU-1998 (REL. 36, LAST ANNOTATION NITRATE REDUCTASE (EC 1.6.6.1) (NR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE; 9135588.
MEDISER I.M., LAZARUS C.M.;
PLANT MOL. BIOL. 15:187-190(1990).
                                                                                                                                                                                                                          MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARYOPHYLLALES; CHENOPODIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 287-926 FROM N.A.
                                                                                                                                                                                                                                                                           Query Match 5.7%;
Best Local Similarity 37.0%;
Matches 27; Conservative
                                                                                                                                                                                                                        103383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 DAIHSDKAKKMLE 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IAYHPGTAWRHLD 73
                                                        NITRATE ASSIMILATION
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                                                                                                                                  434 4
578 5
601 6
918 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                  DISULFID
BINDING
BINDING
SEQUENCE
                                                                               METAL
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                                                                                                              METAL
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US-08-934-254-27.rsp

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BETULA VERRUCOSA (WHITE BIRCH) (BETULA PENDULA).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FAGALES;
BETULACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIEMANN A., BRINKMANN K., HACHTEL W.;
MOL. GEN. GENET. 227:97-105(1991).
-!- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
-!- CAȚALYTIC ACTIVITY: NAD(P)H + NITRATE = NAD(P)(+) + NITRITE +
                                                                                                                                                           547 MNTTSKMYSMSE-VKKHNTADSAWIVVHGNVYNATRFLKDHPGGSDSILINAGTDCTEEF 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 MNTSSKMFSMSE-VKKHNSAESAWIIVHGHIYDCTHFLKDHPGGADSILINAGTDCTEEF 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN. SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
                                                                                                                                                                             H(2)O.

COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FA
COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FA
HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
GROUP IS CALLED CYTOCHROME B-557.

SUBUNIT: HOMODIMER.

- INDUCTION: BY NITRATE.

- SIMILARIY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                1; Gaps
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PIR: $15959; RDBJNH.
HSSP, P17571, 2CND.
PROSITE; PS00191; CYTOCHROME_B5; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
OXIDOREDUCTASE; FLAVOPROTEIN; FAD; NADP; HEME; MOLYBDENUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 MOLYBDENUM-PTERIN (POTENTIAL).
234 MOLYBDENUM-PTERIN (POTENTIAL).
419 INTERCHAIN (POTENTIAL).
533 HEME LIGAND (BY SIMILARITY).
586 HEME LIGAND (BY SIMILARITY).
101002 MW, 3CB0D52F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196; DB 1; Length 898;
Pred. No. 8.35e-16;
21; Mismatches 26; Indels
                                                                                               Length 926;
103970 MY: CBBDEAEG CRC32;

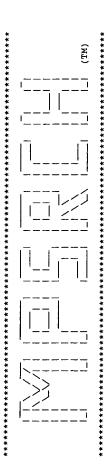
103970 MY: CBBDEAEG CRC32;
                                                                                           Score 199, DB 1; Length 926
Pred. No. 2.39e-16;
19; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE (NAD(P)H) (EC 1.6.6.2) (NR)
                                                                                                                                                                                                                                                                                                                       898 AA.
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.6%;
Best Local Similarity 34.2%;
Matches 25; Conservative
                                                                                           Query Match 5.7%;
Best Local Similarity 37.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                          606 DAIHSDKAKRLLE 618
                                                                                                                                                                                                                                                 61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NITRATE ASSIMILATION
                                             303
926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586
898 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91260687
                                                                                                                                                                                                                                                                                                       RESULT 15
NIA_BETVE
P27783;
                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
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583 DAIHSDKAKKMLE 595

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Qy 61 IAYHPGTAWRHLD 73
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Search completed: Thu Feb 18 11:36:36 1999 Job time : 30 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Feb 18 11:36:54 1999; MasPar time 25.99 Seconds 865.947 Million cell updates/sec

ar output not generated.

>US-08-934-254-27 (1-452) from US08934254.pep 3515 Description: Perfect Score: Sequence: Title:

1 MEGEAKKYITAEDLRRHNKS.....LNSAPCPKKLGYGEAYNTHG 452

PAM 150 Gap 11 Scoring table:

165420 seqs, 49795644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl6
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 49.519; Variance 96.434; scale 0.514 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES			Description
SUMMARIES			Ω
			DB
			No. Score Match Length DB ID
	æ	Query	Match
			Score
_	-	r t	No.

Pred. No.	0.00e+00	0.00e+00	1.11e-58	6.23e-54	1.54e-53	1.70e-36	1.05e-18	1,91e-16	3.04e-15	3.04e-15	3.17e-14	3.17e-14	4.68e-14	4.68e-14	2.20e-13	1.50e-13	3.24e-13	4.76e-13	1.03e-12	4.76e-13
Description	CYTOCHROME B5 CONTAINI	DELTA 6 DESATURASE.	BC269730_2.	DELTA6-FATTY-ACID-DESA	W08D2.4.	T13F2.1.	NITRATE REDUCTASE (FRA	CYTOCHOME B5 (FRAGMENT	NADH NITRATE REDUCTASE	NADH NITRATE REDUCTASE	CYTOCHROME B5 (FRAGMEN	PUTATIVE CYTOCHROME B5	HYPOTHETICAL 48.4 KD P	NITRATE REDUCTASE APOE	DELTA 6 DESATURASE.	NITRATE REDUCTASE (NAD	NITRATE REDUCTASE HEME	CYTOCHROME B5 (FRAGMEN	NITRATE REDUCTASE (EC	NITRATE REDUCTASE (EC
QI	043469	004353	060427	061388	023221	094044	048930	048618	004926	024390	042342	048845	005874	043042	054795	000101	041201	043169	P92922	043265
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% Query Match Length DB	458	448	444	443	473	454	875	134	911	911	113	134	427	915	368	891	74	146	497	501
% Query Match	69.2	60.7	12.3	11.6	11.5	9.0	6.3	5.9	5.7	5.7	5.5	5.5	υ. υ.	5.5	5.4	5.4	5.3	5.3	5.3	5.3
Score	2433	2133	431	407	405	317	220	207	200	200	194	194	193	193	189	190	188	187	185	187
RESULT No.	н	7	ю	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20

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185 182 182 182 182 183 183 177 177 177 176 177 177 177 177 177 177	160 153 153
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ALIGNMENTS

043469, 043469, 04.004-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 06, LAST ANNOTATION UPDATE) 01-TUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) 01-TUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) 01-TUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) 01-TONOTATION PROPERMEN. MELIANTHUS ANNUUS (COMMON SUNFLOWER). ASTERALES; COMPOSITAE. 11 SEQUENCE FROM N.A. STRAIN-CV. INBRED LINE HA89, SF163 /91; TISSUG-COTYLEDONS OF DEVELOPING SUNFLOWER FRUITS; STRAIN-CV. INBRED LINE HA89, SF163 /91; TISSUG-COTYLEDONS OF DEVELOPING SUNFLOWER FRUITS; SPERLING P., SCHWIDT H., HEINZ E.; EUR. J. BIOCHEM. 232:798-805(1995). EMBL: X87143; AG1040729; PFAM: PF00173; hame_1. SEQUENCE 458 AA; 52231 MW; FAZAEZ7B CRC32;	Query Match 69.2%; Score 2433; DB 10; Length 458; Best Local Similarity 66.7%; Pred. No. 0.00e+00; Matches 300; Conservative 92; Mismatches 54; Indels 4; Gaps	13 ADGKKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGQDVTDAFIA 72 ::: :: ::	73 FHPGTAWKHLDKLFTGYH-LKDYQVSDISRDYRKLASEFAKAGMFEKKGHGVIYSLCFVS 131 :	132 LLLSACVYGYLYSGSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIG 191 :::: :: : : : : 123 VMMAAIVYGYLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAG 182	192 NCITGISIAWWKWTHNAHHACNSLDYDPDLQHLPMLAVSKLFNSITSVFYGRQLTFDP 251 :	252 LAREFUSYOHYLYYPIMCVARVNLYLOTILLLISKRKIPDRGLNILGTLIFWTWFPLLVS 311 :1 1:
ULT 043469 043469 01-NOV 01-NO	Query Mat Best Loca Matches					
RESULT 11D 11D 11D 12D 12D 12D 12D 12D	ŌĔ	Db Qy	oy oy	do yo	do y	Oy Oy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 IAGNILTGISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTRLFNSITSVFYGRVLK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSCLPNWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDIS 358
                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                  303 CLPNWPERFGFVLISFAVTAIQHVQFTLNHFSGDTYVGPPKGDNWFEKQTKGTIDITCPP
                                                RLPNWPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFEKQTRGTIDIACSS
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDSLSRFFVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPL
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                                                                                                                                                                                                                                                                                        DOBSON G.
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9
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01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DELTA 6 DESATURASE.
BORAGO OFFICINALIS (BOURRACHE).
BUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
LAMIALES; BORAGINACEAE.
                                                                                                                                                                                                                                                                                                                                                                 Length 448;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                           MEDLINE; 97268723.
SAYANOVA O., SMITH M.A., LAPINSKAS P.A., STOBART SAYANOVA O., SMITH M.A., LAPINSKAS P.A., STOBART CHRESTIE W.W., SHEWRY P.R., NAPIER J.A.;
PROC. NATL. ACAD. SCI. U.S.A. 94:4211-4216(1997).
EMBL: 079010; 62062403; -.
SEQUENCE 448 AA; 51634 WW; 539A4EDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                            onatch 60.7%; Score 2133; DB 10; Local Similarity 57.8%; Pred. No. 0.00e+00; Local Sconservative 105; Mismatches 80
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                                                                                                                                                           448
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|LRDAAVQARDLNSAPCPKKLGYGEAYNTHG 452
                                                                                           LRTAALQARDL-TNPAPQNLAW-EAFNTHG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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444

PRT;

PRELIMINARY;

RESULT 3 ID 060427

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LAMERDIN J.E., MCCREADY P.M., COLEMAN M., SKOWRONSKI E., ADAMSON A.W., BURKHART-SCHULTZ K., GORDON L., KYLE A., RAMIREZ M., STILWAGEN S., BHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J., DANGANNN L., POUNDSTONE P., CHRISTENSEN M., GEORGESCO A., AVILLA J., LIU S., ATTIX C., ANDREISE T., TRANKHEIM M., AMICO-KELLER G., COEFIELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., OUAN G., KROMMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S., KOBAYASHI A., OLSEN A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 VELGK-QK-KKYMPY--NHQHKYFFLIGPPALLPLYFQWYIFYFVIQRKKWV-DLAWM-I 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AFHINKGLVKKYMNSLLIGELSPEQPSFEPTKNKELTDEFRELRATVERMGLM-KANHVF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AYH-P-GTAWRHLDPLFTGYYYLKD--FE-V-S-EISKDYRRLLNEMSRSGIFEKKGHHI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 FLLYLLHILLLDGAAWLTLWVFGTSFLPFLLCAVLLSAVQAQAGWLQHDFGHLSVFSTSK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 T-FYVRFFLTYVP-LLGLKAFLGLFFIVRFLESNWFVWVT-OMNHIP--MHIDHDRNMDW 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 VSTQLQATCNVHKSAFNDWFSGHLNFQIEHHLFPTMPRHNYHKVAPLVQSLCAKHGIEYQ 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 FEKQTKGIIDITCPPWMDWFFGGLQFQLEHHLFPRLPRGQLRKIAPLARDLCKKHGMPYR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 12.3%; Score 431; DB 4; Length 444; Local Similarity 26.8%; Pred. No. 1.11e-58; nes 118; Conservative 112; Mismatches 178; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 QGPTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDATDPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGEAKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 WNHLLHHFVIGH-LKGAPASWWNHMHFQHHAKPNCFRKDPDI-NMHPF-FFA-L-GKILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOBSON G.,
                                                                                                                              CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA;
                                                                                                                                                                                                                                                                                                                                                                                             CARRANO A.V.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; ACO04770; G3169158; -.
SEQUENCE 444 AA; 51964 MW; 6D117044 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 97268723.
SAYANOVA O., SMITH M.A., LAPINSKAS P., STOBART A.K.,
CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;
                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DELTAG-FATTY-ACID-DESATURASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 AA.
       CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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07,
07.
01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
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                                                                                                  HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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SEQUENCE FROM N.A.
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29;

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,

MILSON R., CONNELL M., COPERT T., COOPER J., COULSON A., CRAXTON M.,

DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,

HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAM J.,

AKIRSTEN J., LAISTER N., LAFREILLE P., LIGHTMING J., LLOYD C.,

AKIRSTEN J., ROPRA A., SAUNDERS D., SHOMNERS N., SAALDON N., SMITH A.,

SONNHAAMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,

AVAUDIN M., VAUGHAN K., WATERSTON J., THIERRY-MIEG J., THOMAS K.,

MILKINSON-SPROAT J., WOHLDMAN P.;

H. NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps 16;
                                                                                                                                                                                             Gaps 16;
                                                                                                                                                                                                                                                                                            215 IDHDGDIDLAPLFAFIPGDLCKYKAS-FEKAILKI--VP-YQHLYFT-AMLPMLRFSWTG 269
                                                                                                                                                                                                                                                                                                                   386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLALAWQOFGWLTHEFCHQOPTKNRPLNDTISLFFGNFLQGFSRDWWKDKHNTHHAATNV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 IDHDGDIDLAPLFAFIPGDLCKYKAS-FEKAILKI--VP-YQHLYFT-AMLPMLRFSWTG 299
                                                                                                                                                                                                                                                            147 LLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGNILTGISIAWWKWTHNAHHLACNS 206
                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 VTA-IQHVQFTLNHFSGDIYVGPPKGDNWFEK-QIKGIIDIICPPWMDWFFGGLQFQLEH 377
                                                                                                                                                                                                                            LLALAWQQFGWLTHEFCHQQPTKNRPLNDTISLFFGNFLQGFSRDWWKDKHNTHHAATNV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                    266 LFIQ-TFLLLTRRDVPDR-AL-NLMGIAVFWTW-F-PLFVSCLPNWPERFGFVLIS-FA
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGLLIAHV-VTFNHNSVDKYPANSRILNNFAALQILTTRNMTPSPFIDWLWGGLNYQIEH
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Pred. No. 1.54e-53;
58; Mismatches 121; Indels 18;
                                                                                                                                                        Score 407; DB 5; Length 443;
Pred. No. 6.23e-54;
58; Mismatches 121; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLFPRLPRGQLRKIAPLARDLCKKHGMPYRSFGFWDDANVRTIRTLRDAAVQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLFPTMPRCNLNACVKYVKEWCKENNLPYLVDDYFD-GYAMNLQQLKNMAEH
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SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
U.S.A. 94:4211-4216(1997)
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                                                                  LACEY D.J., SHEWRY P.R.;
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                                                              NAPIER J. A., HEY S.J., LACEY D.J., SHEWRY P.R. BIOCHEM. J. 330:0-0(0).
EMBL, AF031477; G3088520; -.
SEQUENCE 443 AA; 51740 MW; EE44468D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 AA
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07,
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larity 32.5%;
Conservative
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Similarity 32.5%;
95; Conservative
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SCI.
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Best Local Similarity (
Post 95; Conserv
                                                                                                                                                        Query Match
Best Local Similarity
Matches 95; Conserv
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                                SEQUENCE FROM N.A. MEDLINE; 98149727
PROC. NATL. ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-NOV-1996
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W08D2.4.
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SEQUENCE FROM N.A.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
BUTLSON R., AINSCOUGH R., COPERT J., COOLEGN A., CRAXTON M.,
DEAR S., DU Z., DURBLIA N., FAYELLO A., FULTON L., GARDNER A., GREEN P.,
HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
KRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
VANUEN R., VANGHAN K., WATERSTON R., WATSON A., WEINSTOCK E.,
WILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).
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                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMGVAWQQLGWLIHEFAHHQLFKNRYYNDLASYFVGNFLQVSHIFNNGFSSGGWKEQHNV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                 320 VTA-IQHVQFTLNHFSGDTYVGPPKGDNWFEK-QTKGTIDITCPPWMDWFFGGLQFQLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLACNSLDYDPDLQHIPVFA-VSTRLFNSITSVFYGRVLKFDEVAR-FLVSYQHWTYY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 VSHLVGGFLLSHVVTFNHYSVEKFALSSNIMSNYACLQIMTTRNMRPGRFIDWLWGGLNY
                                                             QSVQWVFKENQMEYKVYQRNAFWEQATIVGHWAWVFYQLFL--LPTWPLRVAYFIISQMG
                                                                                                                                                                                         GGLLIAHV-VTFNHNSVDKYPANSRILNNFAALQILTTRNMTPSPFIDWLWGGLNYQIEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHAATNVVGRDGDLDLVPFYATVAEHLNNYSQDSWVMTLFRWQHVHWTFMLPFLRLSWLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 ISFAVTAIQHVQF-TLNHFSGDTYVGPPKGDNWFE-KQTKGTIDITCPPWMDWFFGGLOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
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                                                                                                                                                                                                                                                                                                                                                           Length 454;
                                                                                                                                                                                                                                                                                                                    HLFPTMPRCNLNACMKYVKEWCKENNLPYLVDDYFD-GYAMNLQQLKNMAEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWINBURNE J.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 317; DB 5; Le
Pred. No. 1.70e-36;
75; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53160 MW; D7FD13FA CRC32;
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larity 27.7%;
Conservative
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048930;
01-JUN-1998 (TREMBLREL. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5T 6
Q94044
Q94044;
                                                                                                                                                                                         358
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60 EDVGHSDSAREMMDKYYIG 78
                                        |: :|: :| :|
61 IAY-HPGTAWRHLDPLFTG 78
                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 DAIHSDKAKKLLE 603
                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; PLANTA; EME
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                 004926
004926
004926;
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024390
024390;
                                                                                                                                                    SULTANDA STANDA 
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                                                                                                                     GLYCINE MAX (SOYBEAN).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
FABACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 MNTTSKTYTMSE-VRRHNNADSAWIIVHGHVYDCTRFLKDHPGGTDSILINAGTDCTEEF 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MASDPKIYVY-EEVEKHDKTKDCWLVINGKVYDVTPFMDDHPGGDEVLLSATGKDATNDF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTAE; MITOCHONDRIAL EÚKARYOTES; VIRIDIPLANTAE;
CHAROPHYTA,EMBRYOPHYTA GROUP; EMBRYOPHYTA; VASCULAR PLANTS;
SEED PLANTS; MAGNOLIOPHYTA; MAGNOLIOPSIDA; GENTIANANAE;
SCROPHULARIALES; OLEACERE; OLEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 220; DB 10; Length 87:
Pred. No. 1.05e-18;
16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 207; DB 10; Length 13 larity 36.7%; Pred. No. 1.91e-16; Conservative 20; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CV. KORONEIKI;
MARTSINKOVSKAYA A.I., POGHOSYAN Z.P., HARALAMBIDIS K.G.,
HATZOPOULOS P., MURPHY D.J.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AJ001370; E1216720; -.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
CHYNA B., SMARRELLI J.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. #7027780; G2731816; -.
PROSITE; PSO0191; CYTOCHROME_B5; 1.
PROSITE; PSO0559; MOLYBDOPTERIN_EUK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINSCY. KORONEIKI;
MARTINKOVSKAYA J.:;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
NITRATE REDUCTASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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875
98406 MW; 2CB2F7E7 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AA
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 9612329.
WU S., LU Q., KRIZ A.L., HARPER J.E.
PLANT MOL. BIOL. 29:491-506(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 6.3%;
Similarity 41.1%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -JUN-1998 (TREMBLREL. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOCHOME B5 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 EAIHSDKAKQMLE 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
875 8
875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 29; Conserv
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Best Local Similarity
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NON_TER
SEQUENCE
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048618
048618;
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SUBMITTED (MAR.1997) TO EMBLY-GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ANDPH + NITRATE - NADP(+) + NITRITE + H(2)O.
-!- COFACTOR: FAD; HEME; MOLYBDENUM.
EMBL: U95317; G1946812; -.
PROSITE: PS00191; CYTOCHOME_B5; 1.
PROSITE: PS00159; MOLYBDOPTERIN_EUK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 MNTASKMYSMSE-VRKHNSSDSAWIIVHGHIYDASRFLKDHPGGVDSILINAGTDCTEEF
                                                     01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 04, LAST SANOTATION UPDATE)
NADH NITRATE REDUCTASE (EC 1.6.6.3) (NITRATE REDUCTASE (NADPH)).
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                                                                                                                                                                                                    SOLANUM TUBEROSUM (POTATO).
EURARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TERRINGON, DESIREE;
HARRIS N., FOSTER J.M., KUMAR A., DAVIES H.V., WRAY J.L.;
HARRIS N., FOSTER J.M., KUMAR A., DAVIES H.V., WRAY J.L.;
BUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

REMEL, U76701; G173613; -.
R PROSITE; PS00199; CYTOCHROME B5; 1.
R PROSITE; PS00199; MOLYBDOPTERIN_EUK; 1.
R PFAM; PP00173; Andered_molyb.
R PFAM; PP00175; Oxidored_fad.
N OXIDOREDUCTAGE; HEME.
SEQUENCE 911 AA; 102596 MW; GAECEEC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 200; DB 10; Length 911;
Pred. No. 3.04e-15;
16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 200; DB 10; Length 911;
Pred. No. 3.04e-15;
16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-Jan-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AGG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
NADH NITRATE REDUCTASE (EC 1.6.6.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102609 MW; 44AC790F CRC32;
911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00173; heme_1.
PFAM; PF00174; oxidored_molyb.
PFAM; PF00175; oxidored_fad.
OXIDOREDUCTASE; HEME.
SEQUENCE 911 AA; 102609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.7%;
Best Local Similarity 39.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.7%;
Best Local Similarity 39.7%;
Matches 29; Conservative
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1 MEGEAKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAF
                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL 48.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 VRVREVCDRYDLPYTTGSF 342
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04,
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Best Local Similarity 32.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=TLRL13; TISSUE=LEAF;
SALAMOUBAT M., BUDANG H.D.;
                                                                                                      61 IAY-HPGTAWRHLDPLFTG
                                                             60 EDVGHSESAREMMEQYYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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005874
005874;
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Q43042
Q43042;
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SO CHENE AND CONTROL PROPERTY

SO CHENE AND CONTROL PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                             MNTASKMYSMSE-VRKHNSSDSAWIIVHGHIYDASRFLKDHPGGVDSILINAGTDCTEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 RKVLSFEEVSKHNKTKDCWLIISGKVYDVTPFMDDHPGGDEVLLSSTGKDATNDFEDVGH
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STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC003974; G2914701; -.
PROSITE; PS00191; CYTOCHROME_B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                            C42342
Q42342;
Q42342;
Q42342;
Q1-NOY-1996 (TREMBLREL. 01, CREATED)
O1-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
CYTOCHROME B5 (FRAGMENT).
CYTOCHROME B5 (FRAGMENT).
EUKARIODPSIS THALLANA (MOUSE-EAR CRESS).
EUKARYOTA: PLANIA, EMBRYOPHYTA; ANGIOSPERWAE; DICOTYLEDONEAE; CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA: PLANTA: EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES: CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

5.5%; Score 194; DB 10; Length 134;
Best Local Similarity 38.0%; Pred. No. 3.17e-14;
Matches 30; Conservative 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 194; DB 10; Length 11.
Pred. No. 3.17e-14;
16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUB-CELL SUSPENSION CULTURE OF ECOTYPE COLUMBIA;
CCOKE R., LAUDIE M., RAINAL M., DELSENY M.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; F20001; E225588;
PFAM; PP00173; heme_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66CD71FB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AA.
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113 AA; 12686 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06,
06,
07,
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Best Local Similarity 40.5%;
Matches 30; Conservative
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01-JUN-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE CYTOCHROME B5.
                                                                                                                                                 603
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                                                                                                                                                                                                     61 IAYHPGTAWRHLD 73
                                                                                                                                                 591 DAIHSDKAKKLLE
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NON_TER
SEQUENCE
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048845
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265 FTKTDMIGEPKGQ-WYLRQMLGSANFNAGPALRFMSGNLCHQIEHHLYPDLPSNRLHEIS 323
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9
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NITRATE REDUCTASE APOENZYME (EC 1.6.6.1) (NITRATE REDUCTASE (NADH))
(ASSIMILATORY NITRATE REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.
-i- COFACTOR: FED OR FMN; HEME; MOLYBDENUM.
EMBL; L.11563; 6484212; PROSITE; PSO0191; CYTOCHROME_B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETUNIA HYBRIDA (PETUNIA).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MYCOBACTERIUM TUBERCULOSIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 193, DB 2; Length 427
Pred. No. 4.68e-14;
20; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=H37RV;
COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BADCOCK K., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; 295121; E314467; --
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 AA; 48443 MW; 5D40CA8B CRC32;
                                                                                                                                                                                                                                     427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915 AA
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01-NOV-1996 (TREMBLREL. 01, LAST SEQ0
01-AUG-1998 (TREMBLREL. 07, LAST ANNO
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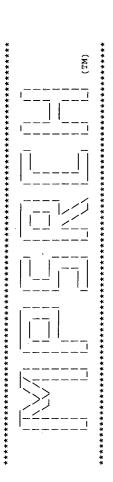
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ij
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                                                                                                                                                                                                                                 Gaps
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                                                                                                                                   Length 915;
                                                                                                                               Query Match
5.5%; Score 193; DB 10; Length 915
Best Local Similarity 37.0%; Pred. No. 4.68e-14;
Matches 27; Conservative 18; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 189; DB 2; Length 368; Best Local Similarity 29.7%; Pred. No. 2.20e-13; Matches 38; Conservative 31; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ITALY;
WINDRAM N., DESHNIUM P., TASAKA Y.;
(IN) HUNG Y., MILLES D.E. (EDS.);
GAMMA-LINOLENIC ACID,
METABOLISM AND ITS ROLES IN NUTRITION AND MEDICINE:22-32;
ACC PRESS, CHAMPAIGN, ILLINOIS (1996).
EMBL; X87094; G809110; -.
SEQUENCE 368 AA; 42083 MW; A9222BFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                            LT 15
054795,
01-NOY-1996 (TREMBLREL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DELTA 6 DESTURASE.
DESTURANCE OF SECURASE.
SPIRGLINA PLATENSIS.
SPIRGLINA PLATENSIS.
SPIRGLINA PLATENSIS.
SPIRGLINA PLATENSIS.
CYANOBACTERIA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); OSCILLATORIALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
             PFAM; PF00173; heme_1.
PFAM; PF00174; oxidored_molyb.
PFAM; PF00175; oxidored_fad.
OXIDOREDUCTASE; HEWE.
SEQUENCE 915 AA; 103037 MW; 17A4F657 CRC32;
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
                                                                                                                                                                                                                                                                                    596 DAIHSDKAKKLLE 608
                                                                                                                                                                                                                                                                                                           | |: |: |:
61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Oy 399 CKKHGMPY 406
Search completed: Thu Feb 18 11:37:56 1999
Job time: 62 secs.

327 CEEFGVNY 334

8 % B



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 13.14 Seconds 556.518 Million cell updates/sec Thu Feb 18 11:33:50 1999; Run on:

ar output not generated.

(1-452) from US08934254.pep 3515 >US-08-934-254-27 Description: Perfect Score: Title:

1 MEGEAKKYITAEDLRRHNKS......LNSAPCPKKLGYGEAYNTHG 452

Scoring table:

Sequence:

131922 segs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq32
lipart1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part1 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 22.part22 23.part23
24.part24 25.part25 26.part26 27.part27 28.part28
29.part29

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scale 0.231 Variance 155.761; Mean 36.009; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match	% Query Match Length	E E	E	Description	, ON
		3 :			
	448	18	R98455	Borage delta-6-desatu	4.05e-194
	899	17	R90987	Nitrate reductase.	7.83e-08
	911	7	R10333	Deduced sequence of t	2.08e-07
	904	œ	R41757	Nitrate reductase Nia	8.15e-07
	130	23	W22848	Mortierella alpina cy	1.77e-06
	66	11	R57734	Pre-apo-protein encod	2.52e-04
	121	11	R57732	Pre-apo-protein encod	2.52e-04
	156	11	R57733	Pre-apo-protein encod	2.52e-04
	359	^	R34102	Bacterial delta-6-des	6.41e - 04
	359	18	R98456	Synechocystis delta-6	1.12e-03
	437	25	W24134	Fructosyl amino acid	8.96e+00
	847	15	R88320	IL-4 Stat peptide.	1.24e+01
	176	m	R13988	Beta-carotene hydroxy	2.79e + 01
	2317	Н	P92219	CR1 protein	2.79e+01
	1594	Ŋ	P81184	Sequence encoded by t	4.49e+01
	266	56	W21774	Protein encoded by OR	8.39e+01
	266	56	W21775	Protein encoded by OR	8.39e+01
	288	13	R66476	Wild type human epimo	7.19e+01

Length 448;

Score 2134; DB 18; Pred. No. 4.05e-194;

60.7%; 57.8%;

Query Match Best Local Similarity

.396+ .396+ .396+	900 t		146644	
rphin. tainin id-des n sens n resi	e of fro 3CGS	Cyclic-GMP-stimulated Cyclic-GMP stimulated Cyclic GMP stimulated cGS-PDE amino acid se	fish shark kidney uence encoded by pylori secreted o erferon induced 1 nocated HSV specif	Truncated HSV specifi Truncated HSV specifi Truncated HSV specifi Truncated HSV specifi Truncated HSV specifi Truncated HSV specifi Truncated HSV specifi Sequence of gpJ encod
365 513 605 881 881	7007	W18048 R69728 W11239 W18049	* • • • • • • • • •	6664 6664 6663 6663
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4 4 1 1 0 4 4 2 2 2 4 4 2 2 2 2 2 2 2 2 2 2 2 2	921 921 921	0 0 0 0 0 0 4 4 0 0 1 2 2 2 2	1026 1026 1109 125 352	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
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ALIGNMENTS

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Transgenic plants comprising the borage delta-6-desaturase gene-
for any increased production of gamma linolenic acid and having
for increased resistance to chilling
for increased resistance to chilling
for increased resistance to chilling
for increased resistance (as partial for the following for form a borage membrane-bound polysomal library. The sequence is distinct from that of five following following for the following following for the following for the following for the following following for following following for following fo
                                                                                                                                                   transgenic plant; borage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas TL;
                                                                                                                 Borage delta-6-desaturasé.
Delta-6-desaturase, gamma-linolenic acid; transgenic
polyunsaturated fatty acid; octadecatetraeonic acid;
chilling resistance; oilseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reddy AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nunberg AN,
                                                                                                                                                                                                                                                                                                156..163
/label= Lipid_box
196..200
/label= Metal_box-1
372..377
/label= Metal_box-2
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1995; IB1167.
30-DEC-1994; US-366779.
(RHON ) RHONE POULENC AGROCHIMIE.
                                 AA.
nr 1
898455;
R98455;
15-SEP-1996 (first entry)
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WPI; 96-333997/33.
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Matches

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(INRG ) INRA INST NAT RECH AGRONOMIQUE.
 911 AA.
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R41757 standard; Protein; 904 AA.
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ilarity 39.7%;
Conservative
                                                                                             18-JUL-1990; 402077.
19-JUL-1989; FR-009707.
(INRG ) INST NAT RECH AGRON.
Daniel-Vedele F, Caboche M;
 standard; Protein;
                                                          Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1993.
05-MAR-1993; F00222.
05-MAR-1992; FR-002658.
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les 29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vincentz M;
WPI; 93-303468/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09318154-A
                                                                                    23-JAN-1991
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nitrogen
9
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Nitrate reductase; populus nigar; absorbtion; nitrogen oxide; pollutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus sp. nitrate reductase gene - useful for generating transgenic plants with enhanced nitrogen oxide absorbing activity claim 1, Page 4-8; 9pp; Japanese.
This sequence represents the nitrate reductase sequence obtained from Populus nigra L. The gene encoding this sequence can be used to gener plants, especially trees, having enhanced activity for absorbing nitro
                                                                     180 IAGNILTGISIAMWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTRLFNSITSVFYGRVLK 239
                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                 417
                                                                                                                                                                                                                                                                                                                             527 mntssktfsmae-vkkhnsadsawiivhghvydctrflkdhpggtdsilinagtdcteef 585
                                  Gaps
                       maaqikkyitsdelknhdkpgdlwisiqgkaydvsdwvkdhpggsfplkslagqevtdaf
                                                                                                                  flaml fams vygvl fcegvlvhl fsgclmg flwigsgwighdaghymvvsdsrlnk fmgi
                                                                                                                                                                   faanclsgisigwwkwnhnahhiacnsleydpdlgyipflvvsskffgsltshfyekrlt
                                                                                                                                                                                                                               299 lvsclpnwgerimfviaslsvtgmgqvqfslnhfsssvyvgkpkgnnwfekqtdgtldis
                                                                                                                                                                                                                                                                              fdslsrffvsyqhwtfypimcaarlnmyvqslimlltkrnvsyraqellgclvfsiwypl
                                                                                                                                                                                                                                                                                                                 cppwmdwfhgglqfqiehhlfpkmprcnlrkispyvielckkhnlpy-nyasfskanemt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 205, DB 17; Length 89
Pred. No. 7.83e-08;
17; Mismatches 27; Indels
Indels
80;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                            418 Irtlrntalgarditk-plpknlvw-ealhthg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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14-JUL-1994; JP-162197.
(TOYW) TOYOTA CHUO KENKYUSHO KK.
(TOYN) TOYOTA JIDOSHA KK.
WPI; 96-133419/14.
Conservative 105;
                                                                                                                                                                                                                                                                                                                                                                                                                          T
R90987 standard; Protein; 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
llarity 38.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 daihsdkakkmle 598
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|IAYHPGTAWRHLD 73
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tes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            899 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxide pollutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Populus nigra.
J08023978-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches

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RESULT

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Claim 2; Fig 1; 27pp; French.

Chaim 2; Fig 1; 27pp; French.

Chaim 2; Fig 1; 27pp; French.

Chaim Ecott digest of formato DNA was screened with labelled tobacco nitrate reductase cDNA under low stringency conditions. A 6.5% fragment contained part of the tomato nitrate reductase gene and was used, under high stringency, to screen a Hind III library. A 7kb fragment was isolated, having 1.5kb in common with the Econi fragment. Restriction fragments were subcloned and sequence. The fragment. Restriction fragments were subcloned and sequence. The known nitrate reductases from other plants, eg. Nicotiana, Solanum, Trifolium pratense, Cucumis sativus, etc., shows conserved regions. These have structural and/or functional importance and cred to be separated by variable regions, often hydrophilic, which sequence 911 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 mntaskmysmse-vrkhnssdsawiivhghiydasrflkdhpggvdsilinagtdcteef 590
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Overexpression of nitrate reductase (NR) can stimulate the early development of plants, shortening the duration of the vegetative phase and causing earlier germination, flowering and ripening by about two weeks. Overexpression of NR can also cause the level of nitrate stored in a plant to be reduced, reducing risks to health and also possibly improving organoleptic qualities. The NR gene w introduced into plants by transforming a strain of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R41757;
21-MAR-1994 (first entry)
Nitrate reductase Nia2 derivative.
Nitrate reductase, germination; flowering; ripening; development;
growth stimulation; Agrobacterium tumefaciens; nitrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing over-expression of nitrate reductase in plants. - esp. by incorporation of foreign gene, for stimulating early development and reducing nitrate accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 91-024287/04.

PSDB; 910280.

New DNA encoding tomato nitrate reductase - and related cloning and expression vectors, used to improve nitrogen assimilation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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Pred. No. 2.08e-07;
16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dorlhac F, Morot-gaudry
08-APR-1991 (first entry)
Deduced sequence of tomato nitrate reductase.
tomato nitrate reductase; nitrogen assimilation.
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its inhibitors
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                                                                                                                                                                   527 mntaskmysmse-vrkhssadsawiivhghiydatrflkdhpggtdsilinagtdcteef 585
                                                                                                                                                                                           Mortierella alpina cytochrome b5 (cytb5) gene - used for recombinant production of cytb5 which is used in the preparation of essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 aelksf-tladlsghttkdslylaihgkvydctgfidehpggeevlideagrdatesfed 60
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                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatty acids
Claim 3; Page 11; 14pp; Japanese.
The present sequence is the Mortierella alpina cytochrome b5
(cytb5), useful for the efficient preparation of human essential
fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 94-264104/32.
N-PSDB: 067222.
Genetic precure unit causing periplasmic translocation of
pre-apo-protein - for processing the halo-protein, useful in
protein synthesis, assay of signal peptidase and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
  tumefaciens with a plasmid and using it to infect the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; Length 130;
                                                                                   Length 904;
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                                                                              Score 193; DB 8; Length 904
Pred. No. 8.15e-07;
19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mortierella alpina cytochrome b5.
Cytochrome b5; cytb5; preparation; production; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 189; DB 23;
Pred. No. 1.77e-06;
                                                                                                                                                                                                                                                                                                                                                  .r 5
W22848 standard; Protein; 130 AA.
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Local Similarity 38.0%;
les 30; Conservative
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27-JAN-1993; GB-001553.
(UYWA-) UNIV COLLEGE WALES.
                                                                              Match 5.5%;
Local Similarity 35.6%;
les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1997.
01-AUG-1996; 203735.
01-AUG-1995; JP-196868.
(SUNR.) SUNTORY LTD.
WPI; 97-314231/29.
                                                                                                                                                                                                                                                  586 daihsdkakklle 598
                                                                                                                                                                                                                                                                                           61 IAYHPGTAWRHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fátty acid.
Mortierella alpina.
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                                          904 AA;
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                     plant(s).
                                        Sequence
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Claim 10; Fig. 4; 32pp; English.

This sequence encodes the pre-form of an apo-protein. The pre-apo-
protein is translocated from a cytoplasmic cell region to a
periplasmic region where formation of process apo-protein and
conversion to halo-protein occur. The protein is expressed in the
cytoplasm of E. coli, especially fall and N4830-1. The apo-protein
is a cytoplasmic cytochrome, especially having a soluble core domain
of cytochrome-b5 of liver endoplasmic reticulum.
                                               This sequence encodes the pre-form of an apo-protein. The pre-apo-protein is translocated from a cytoplasmic cell region to a periplasmic region where formation of process apo-protein and conversion to halo-protein occur. The protein is expressed in the cytoplasm of E. coli, especially TB-1 and N4830-1. The apo-protein is a cytoplasmic cytochrome, especially having a soluble core domain of cytochrome-b5 of liver endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                  10 kyytleeiqkhkdskstwvilhhkvydltkfleehpggeevlreqaggdatenfedvghs 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 kyytleeiqkhkdskstwvilhhkvydltkfleehpggeevlreqaggdatenfedvghs 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pre-apo-protein – for processing the halo-protein, useful in
protein synthesis, assay of signal peptidase and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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    1..22
/note= "alkaline phosphatase signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1995 (first entry)
Plasmid pAA-cyt.
Plasmid pAA-cyt.
Plasmid pAA-cyt, vector; holo-protein; pre-apo-protein;
protein synthesis; Escherichia coli; cytoplasm cytochrome.
                                                                                                                                                                                                                                                                                                                 Length 99;
                                                                                                                                                                                                                                                                                                              Score 163; DB 11; Length 99
Pred. No. 2.52e-04;
13; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "soluble core of cytochrome-b5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 163; DB 11;
Pred. No. 2.52e-04;
13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T. 7
R57732 standard; Protein; 121 AA.
of its inhibitors
Claim 10; Fig.6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic precursor unit causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.6%;
Best Local Similarity 37.1%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.1%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1993; GB-001553.
(UYWA-) UNIV COLLEGE WALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-1994; G00161.
27-JAN-1993; GB-0015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 tdarelskty 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 TAWRHLDPLF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 tdarelskty 79
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Pred. No. 6.41e-04;
16; Mismatches 35;
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Pred. No. 1.12e-03;
16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuccio M, Nunberg AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Metal_box-1
302..307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85..92
/label= Lipid_box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1996 (first entry)
Synechocystis delta-6-desaturase.
                                                                                                                                                                                                                                                                                                                                                                           .T 10
R98456 standard; Protein; 359 AA.
R98456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RHON ) RHONE POULENC AGROCHIMIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W24134 standard; Protein; 437 AA.
                                                                                                                                                                                                                                                                                  403 GMPYRSFGFWDDANVRIIR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.4%;
Best Local Similarity 32.8%;
Matches 22; Conservative
Best Local Similarity 31.6%;
Matches 25; Conservative
                                                                                                                                                                                                                     332 gveykvyptfkaaiastyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123..128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-1996.
28-DEC-1995; IB1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freyssinet GL, Nu.
WPI; 96-333997/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 gveykvy 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 GMPYRSF 409
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Disclosure; Page 30-33; 45pp; English.
Providing the gene (1) encoding delta-6-desaturase, allows prodn. of transgenic organisms which contain functional delta-6-desaturase and which produce gamma-linolenic acid (GLA). In addition to allowing prodn. of large amts. of GLA, a new dietary source of GLA is provided. Chilling tolerance may be introduced in plants by introduction of (1) into a plant cell and regeneration of a plant with improved chilling resistance from the transformed plant cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic precursor unit causing periplasmic translocation of pre-apo-protein of prevences of processing the halo-protein, useful in protein synthesis, assay of signal peptidase and identification of its inhibitors of its inhibitors.

This sequence encodes the pre-form of an apo-protein. The pre-apo-protein is translocated from a cytoplasmic cell region to a periplasmic region where formation of process apo-protein and conversion to halo-protein occur. The protein is expressed in the cytoplasmic cytoplasmic cytoplasmic cytoplasmic cytoplasmic sepecially TB-1 and N4830-1. The apo-protein of cytoplasmic cytochrome, especially having a soluble core domain of cytochrome-b5 of liver endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gamma-linolenic acid; GLA; linoleic acid; diet; chilling tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 kyytleeigkhkdskstwvilhhkvydltkfleehpggeevlregaggdatenfedvghs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
                                                            24-MAR-1995 (first entry)
Pre-apo-protein encoded by plasmid pSEC-cyt/c.
Plasmid pSEC-cyt/c; vector; holo-protein; pre-apo-protein; protein synthesis; Escherichia coli; cytoplasm cytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; Score 158; DB 7; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 163; DB 11;
Pred. No. 2.52e-04;
13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocysistis (PCC 6803, ATCC 27184).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reddy AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR.1993.
13-OCT-1992; U08746.
13-OCT-1991; US-774475.
08-JAN-1992; US-817919.
(RHON ) RHONE POULENC AGROCHIMIE.
Freyssinet G, Nuccio M, Reddy AS,
WPI: 93-134023/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R34102 standard; Protein; 359 AA.
R34102;
      R57733 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial delta-6-desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.6%;
Best Local Similarity 37.1%;
Matches 26; Conservative
                                                                                                                                                                                                                                                  04-AUG-1994.
27-JAN-1994; G00161.
27-JAN-1993; GB-001553.
(UTWA-) UNIV COLLEGE WALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAWRHLDPLF 76
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 94-264104/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 AA;
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                                                                                                                                                                                                                                                                                                                                                                           Kaderbhai MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1993
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                                                           dewaicgirttanfatnnpfw-nwfcgglnhqvthhlfpnichihypqleniikdvcqef 331
                                                                                               273 dewaicgirttanfatnnpfw-nwfcgglnhqvthhlfpnichihypgleniikdvcqef 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage; polyunsaturated fatty acid; octadecatetraeonic acid; chilling resistance; oilseed. Synechocystis sp. strain PCC 6803 (ATCC 27184).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased resistance. Loud out gamma innolenic acid and having increased resistance to chilling Disclosure; page 48-49; 75pp; English. Synechocystis sp. PCC 6803 delta-6-desaturase (R98456) catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It sequence was deduced from that of the delta-6-desaturase gene (T30396) isolated from a Synechocystis cosmid genomic library. The sequence is distinct from that of borage delta-6-desaturase (R98455). Expression of the desaturase in bacteria, fund, animals or plants results in increased GLA prodn. Alteration of the desaturase may result in increased resistance to chilling. Sequence 359 AA;
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16-FEB-1998 (first entry)
Fructosyl amino acid oxidase.
Fructosyl amino acid oxidase; FAOD-P; enzyme; amadori compound; alpha-ketoaldehyde amine derivative; amadori detection.
Penicillium janthinellum.
W09721818-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plants comprising the borage delta-6-desaturase show increased production of gamma linolenic acid and havir
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                          R13988 standard; Protein; 176 AA.
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P92219 standard; protein; 2317.
P92219;
22-FBB-1990 (first entry)
CRI protein
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VGHDSGHYQVMPTRGY-NRI 176
   Query Match 2.9%;
Best Local Similarity 21.1%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7. Match 2.8%;
Local Similarity 28.8%;
les 23; Conservative
                                                                                                                                                                                                                                       26-NOV-1991 (first entry)
                                                                                                                                                                                                                                                        Beta-carotene hydroxylase
                                                                                                                                                                                                                                                                                                                           04-AUG-1991; U01458.
02-MAR-1990; WO-487613.
18-MAY-1990; US-525551.
03-AUG-1990; US-562674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                 91-281410/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        respectively.
                                                                                                                                                                                                                                                                                                WO9113078-A.
                                                                                                                                                                                                                                                                                                                 05-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                             433
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                                                                                                                related DNA - used for detection of amadori compounds in foods and claim body fluids such as blood claim 1; Pages 33-36; Sapp, Japanese.

This sequence represents the fructosyl amino acid oxidase (FAOD-P) of the invention. This sequence was isolated from Penicillium janthinellum 5.3413 (FERM BP-5475). FAOD-P oxidises amadori compounds in the presence of oxygen, producing alpha-ketoaldehyde, amine derivatives and hydrogen peroxide. FAOD-P is used in the detection of amadori compounds in, e.g. foods such as soy sauce, and in body fluids such as blood. This sequence, vectors containing it and host cells transformed by the vector are all sequence 437 AA;
                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                      dsghsfkvlpnig-khvveliegrlpqdlagaw-rwrpggdalkskrsapakdlaempgw 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure: Page 17-19; 22pp; English.

Interleukin-4 signal transducer and activator of transcription (IL-4 star) (R88320) is a movel transcription factor characterized by selective binding to intracellular domains of cytokine receptors. It was obtd. by expression of a cDNA clone (T03679) isolated from human monocytic Thp-1 cells. The IL-4 Stat peptide is used to identify cpds. useful in the treatment/diagnosis of immune diseases, bacterial, viral or fungal infections, metabolic or genetic diseases, neoplasia, inflammation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-4 signal transducer and activator of transcription (IL-4 Stat) peptide(s) - bind to natural intracellular IL-4 Stat binding target and are useful to identify cpds. for treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                    Fructosyl amino acid oxidase which oxidises amadori compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amino acids 401-650 constitute an active IL-4 Stat peptide (Claim 3, page 21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-4 Stat peptide.
Interleukin-4 signal transducer and activator of transcription;
                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //note= "amino acids 1-40 constitute an active
II-4 Stat peptide (Claim 2, page 21)"
                                                                                                                                                                                                                                                                                                              Length 437;
                                                                                                                                                                                                                                                                                                            Score 104; DB 25; Length 43
Pred. No. 8.96e+00;
15; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stat; transcription factor; immunosuppressive
                                                            Tani Y;
                                          (KYOT-) KYOTO DAIICHI KAGAKU CO LTD.
Fukuya H, Kato N, Sakai Y, Tani Y
WPI: 97-32789/30.
N-PSDB; T85703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R88320 standard; Protein; 847 AA.
                                                                                                                                                                                                                                                                                                           Match 3.0%;
Local Similarity 27.3%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-Jan-1996.
05-JUL-1995; 304715.
05-JUL-1994; US-269604.
15-JUL-1994; US-276099.
(TULA-) TULARIK INC.
WPI. 96-070143/08.
N-PSDB: T03679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401..650
19-JUN-1997.
13-DEC-1996; J03651.
14-DEC-1995; JP-325672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                             432 khdakl 437
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                                                                                                                                                                                                                                                                                                           ery Match
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                                                                                                                                                                                                                                                                                                                                         Matches
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ID R8
AC 29
DF 29
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KW II
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                                                                                                                                                                                                                                                                                                                  semdrvp-fvvaervpwekmcetlnlkfmaevgtnrgllp-ehflflagkifndnslsme 490
                                                                                                                                                                                                                                                                                                                                                                                                         211 PDLQHIPVFAVSTRL-FNSITSVFYGRVLKFDEVARFLVSYQHWTYYPVMIFGRVNLFIQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 NEMSRSGIFEKKGHHIMWTFVGVAVMMAAI-VYGVLASESVGVHMLCGALLGLLWIQAAY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 hhtprkgvfelndlfav-vfagvaialiavgtagvwplqwigcgmtvygllyfl-vhdgl 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The native sequence (Q13724) was genetically engineered. At the 5' end of the gene, codons encoding the native second and third amino acid have been changed from Leu-Val to Val-Leu. Recombinant expression plasmids can be used to produce ants. of the enzymes and hence large amts. of the carotenoids which they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 102; DB 15; Length 847;
Pred. No. 1.24e+01;
36; Mismatches 44; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ر.
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Biosynthesis of carotenoid(s) in genetically engineered hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 afghrsvswsqfnkei-llgrgftfwqwfdgvldltkrclrsywsdrliigfis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STAD ) AMOCO CORP.
Ausich RL, Brinkhaus FL, Mukharji I, Proffitt JH, Yarger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 3; Length 176;
Pred. No. 2.79e+01;
22; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss
Erwinia herbicola EHO-10 (E. vulneris - ATCC 39368).

    variant.

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                                                                                                                                                                                                                                                                             Homo sapiens (human)
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No responsibility of the property of the protein of the fragment, but inflammation, myocardial infarct, etc.

To diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc.

Tin inflammation, myocardial infarct, etc.

This is full-length CRI protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity.

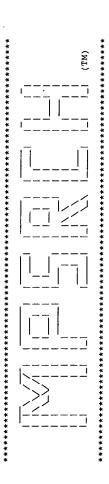
In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and prevent perfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2192 nyatyxxpllifxfifcl-ssftyvff-yirtfpplvcfllfyra-epysfkgf-rvkym 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide. The extreme carboxy-terminal part comprises a region of 20 hydrophobic AAs, which presumably serves as a transmembrane anchor. The FIPV peplomeric protein has 35 potential glycosylation sites, of which 22 are in the N-terminal part (pos. 1-790) which corresponds to the S-part of the IBV E2 (see P01183). N.B. IBV = infectious bronchitis virus. "X" in the AA sequence denotes the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 DYDPDLQHIPVFAVSTRLFNSITSVFYGRVLKFDEVARFLVSYQHWTYYPVMIFGRVNLF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weel for feline infectious peritonitis virus - and gene prod. useful as antigenic protein for vaccine Disclosure; Fig 1; 13pp; English. Disclosure; Fig 1; 13pp; English. obtain 79-1146. N81533 gives the sequence of the peptomeric gene in three reading frames. The top reading frame is an open reading frame of 4356 nucleotides and has a coding capacity for a precursor polypeptide having a mol. wt. of 160,470 (1452 AAs). The beginning and the end of the E2 gene are indicated in the FT of N81533. The first 18 N-terminal AAs have a strong hydrophobic character and presumably comprise a cleavable signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Gaps
                                                                                                            01-APR-1988; US-176532.
(TCEL) T Cell Sciences Inc; (UVJO) The Johns Hopkins University;
(RBIG*) The Brigham and Women's Hospital.
Fearon DT, Klickstein LB, Wong W, Carson G, Concino MF, Makrides SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Policy., 29-007-1992 (first entry)
Sequence encoded by the 2nd reading frame of the peplomeric gene of FIVP strain 79-1146.
Vaccine, peplomeric protein, E2 gene.
Feline infectious peritonitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%; Score 97; DB 1; Length 2317; Best Local Similarity 27.9%; Pred. No. 2.79e+01; Matches 24; Conservative 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-1987; 201657.
05-SEP-1986, NL-002244.
(DUIN ) DUPHAR INT RES BV.
De Groot RJ, Spaan WJM, Van Der Zeijst BAM; NPI; 88-114447/17.
N-PSDB; N91533.
10..50
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2248 lyqfllslgrkinllerhemimgrvv 2273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               т 15
P81184 standard; Protein; 1594 AA.
                                                                                           31-MAR-1989; U01358
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Sequence 1594
                                                                                                                                                                                                                               N-PSDB; N91477
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29-0CT-1992
  peptide
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Query Match 2.7%; Score 94; DB 5; Length 1594;
Best Local Similarity 26.4%; Pred. No. 4.49e+01;
Matches 24; Conservative 24; Mismatches 36; Indels 7; Gaps 7;
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873 xlpltvncxvxhigqrhlifittlyiitqvr 903

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Search completed: Thu Feb 18 11:34:58 1999 Job time : 68 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Feb 18 11:38:16 1999; MasPar time 6.00 Seconds 712.828 Million cell updates/sec lar output not generated. Run on:

>US-08-934-254-27 (1-452) from US08934254.pep 3515 1 MEGEAKKYITAEDLRRHNKS......LNSAPCPKKLGYGEAYNTHG 452 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

100342 seqs, 9469514 residues Searched:

Database:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Mean 33.831; Variance 160.640; scale 0.211 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ħ	ID US-08-366 US-08-366	Description Sequence 5, Applicatio	Pred. No. 1.93e-176
5.3 155	8	Sequence 1,	6.01e-06
4.9 134 2 4.8 142 2	US-08-801 US-08-801	 Sequence 4, Applicatio Sequence 3, Applicatio 	1.03e-04 1.22e-04
	US-08-366	Sequence 2,	1.67e-03
	US-08-307	Sequence 2,	1.67e-03
4.4 359 1	US-08-478	- Sequence 2,	1.67e-03
4.4 359 1 3.9 104 2	US-08-473 US-08-801	 Sequence 2, Sequence 5, 	1.67e-03 3.57e-02
2.9 847	US-08-781	- Sequence 2,	1.01e+01
<u>ه</u> . د	US-08-276	- Sequence 2,	1.01e+01
2.8 175	US-08-624	- Sequence 6, A	2.17e+01
2.6 288 2	US-08-036 US-08-628	 Sequence 18, Applicati Sequence 3, Applicatio 	2.17e+01 5.33e+01
. 6 288	US-08-690	- Sequence 3,	
.6 418	PCT-US94	0 Sequence 72,	5.33e+01
φ.	US-08-818	- Seguence 6,	3.96e+01
.6 473	US-08-439	- Seguence 4,	5.33e+01
۰.	US-08-440	 Sequence 3, 	5.33e + 01
.6 55	US-08-565	- Seguence 6,	3.96e+01
2.6 921 3	PCT-US92-0	Seguence 39,	6.17e+01

24 90 2.6 921 2 US-08-455- Sequence 39, Applicati 6.17e+01 2 0 2.6 921 1 US-08-297- Sequence 39, Applicati 6.17e+01 2 0 2.6 921 2 US-08-455- Sequence 39, Applicati 6.17e+01 2 0 2.6 921 2 US-08-455- Sequence 39, Applicati 6.17e+01 2 0 2.6 921 1 US-07-872- Sequence 39, Applicati 6.17e+01 3 0 0 2.6 942 1 US-07-872- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 1 US-07-872- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 1 US-07-872- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-457- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-457- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-479- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-479- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-479- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-479- Sequence 43, Applicati 6.17e+01 3 0 0 2.6 942 2 US-08-479- Sequence 44, Applicati 6.17e+01 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGNMENTS RESULT 11
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                                                                                                                                                                       119 FIAMLFAMSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGI 178
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                                                                                                  Gaps
                                                                                         1 MAAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAF
                                                                                                                                                                                                               179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT
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Patent No. 578920
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Freyssinet, Georges L.
APPLICANT: Freyssinet, Georges L.
APPLICANT: Preyssinet, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID.
TITLE OF INVENTION: DELTA 6-DESATURASE
                                                  Length 448;
                                                y Match 60.3%; Score 2121; DB 1; Length 44 Local Similarity 57.6%; Pred. No. 1.93e-176; nes 261; Conservative 105; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                          448 AA
                                                                                                                                                                                                                                                                                                                                                                             418 LRTLRNTALQARDITK-PLPKNLVW-EALHTHG 448
                                                                                                                                                                                                                                                                                                                                                                                         :||||::|:||||: | ||:| || :||| 452
        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
JENCE 448 AA; 51599 WW; 1110962 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08789936
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CITY: Garden City
amino acid
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                              SEQUENCE
                                                  Query Match
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                                                            Best Loca
Matches
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120 GVAVMMAAIVYGVLASESVGVHMLCGALLGLLMIQAAYVGHDSGHYQVMPTRGYNRITQL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 FIAMLFAMSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 FDSLSRFFVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPL
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PatentIn Release #1.0, Version #1.25
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Best Local Similarity 57.6%; Pred. No. 1.93e-176;
Matches 261; Conservative 105; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
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28-JAN-1997
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                                                                                                                                                                         CLASSIFICATION: 4.0

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTONEY/AGENT INFORMATION:
NAME: PRESSEY, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXI
TELEPHONE: (516) 742-4443
TELEPHONE: (516) 742-4443
TELEFAX: (516) 742-4366
TELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 AA; 51599 MW; 1110962 CN;
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Patent No. 5831018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08801972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
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                                       CURRENT APPLICATION DATA
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                    CLASSIFICATION:
                                                                                                                         FILING DATE:
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SOFTWARE:
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US-08-801-972-1
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10 KYYTLEEIKKHNHSKSTWLILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHS 69
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Patent No. 5831018
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME
TITLE OF INVENTION: B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA.
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0216 US
TELEPHONE: 415-855-055
TELEPANN: 415-855-055
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: Genbank
CLONE: 476415
NCE 134 AA; 15349 MW; 97278 CN;
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                                                                                                             Diskette
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TOPOLOGY: linear
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                         94304
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                                    COUNTRY:
          STATE:
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Pred. No. 6.01e-06;
16; Mismatches 28; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:

MEDIUM TYPE: Dissette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REF
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Patent No. 5831018
GENERAL INFORMATION:
APPLICANT: GO11, Surya K.
TITLE OF INVENTION: B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
APPLICANT: GOL1, SULYA K.

TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME
TITLE OF INVENTION: B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.3%;
Best Local Similarity 37.5%;
Matches 27; Conservative
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CLONE: 2264814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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67 TAWRHLDPLFTG 78
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REFERENCE/DOCKET NUMBER: 83
        ATTORNEY/AGENT INFORMATION:
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XX XXXXXX
XX Sequence 2, Appliance 3, Applicant: The Applicant The Applicant: The Applicant The Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Necdo, Michael
APPLICANT: Nuccio, Michael
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 170; DB 2; Length 142;
Pred. No. 1.22e-04;
12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 AA
                                                                            APPLICALLON ...
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REERERENCE/DOCKET NUMBER: PF-0216 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acids
TYPE: amino acids
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AA; 16243 MW; 109747 CN;
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                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 39.7%;
Matches 29; Conservative
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CLONE: 703083
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APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Nuccio, Michael
APPLICANT: Nuccio, Michael
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STREET: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                           / Match 4.4%; Score 155; DB 1; Length 359; Local Similarity 32.8%; Pred. No. 1.67e-03; hes 22; Conservative 16; Mismatches 26; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 AA.
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 19,827
RELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83832XXW
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 359 AA; 41425 MW; 698417 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
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REGISTRATION NUMBER: 19,827
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SEQUENCE
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                                                                                                                                                                          Gaps
                                                                                                                                                                        3;
                                                                                                                                            Score 155; DB 2; Length 359;
Pred. No. 1.67e-03;
16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,382
FILING DATE: 14-SEP-1994
CLASSIFICATION: BOTO
PRIOR APPLICATION: BOTO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN.1992
ATTORNEY/AGENT INFORMATION:
NAME: MCNULLY, WILLIAM E.
NAME: MCNULLY, WILLIAM E.
REGISTRATION NUMBER: 22,6065
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08307382
Patent No. 5552306
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Reddy, Avutu S.
APPLICANT: Freyssinet, Georges L.
TILLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                               359 AA
                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 359 AA; 41425 MW; 698417 CN;
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08307382
TELEPHONE: (516) 742-4343
TELERAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: United States
                                                                                                                                            / Match 4.4%;
Local Similarity 32.8%;
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: Scully, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 11530
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403 GMPYRSF 409
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US-08-307-382-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                    SEQUENCE
                                                                                                                                            Query Match
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Matches
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                                                                                                                                Query Match 4.4%; Score 155; DB 1; Length 359; Best Local Similarity 32.8%; Pred. No. 1.67e-03; Matches 22; Conservative 16; Mismatches 26; Indels
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CITY: GATGED CLLY FLAZA
STATE: New YOIK
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,727
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/307,382
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 08/307,382
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 08/307,382
FILING DATE: US SEP-1994
APPLICATION NUMBER: US 07/817,919
FILING DATE: US STAN-1992
ATTONENEY/AGENT INFORMATION:
ANALY: MANAT: LEGISTER
ANALY: LEGISTER
AN
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APPLICANT: Thomas, Terry L.
APPLICANT: Thomas, Terry L.
APPLICANT: Redgy, Avenus S.
APPLICANT: Nuccio, Michael
APPLICANT: Freyssinet, Georges L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Gaiden City Plaza
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FINCE 359 AA; 41425 MW; 698417 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
JENCE 359 AA; 41425 MW; 698417 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08478727
Patent No. 5663068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08478727
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TELEFAX: (516) 742-4366
TELEX: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MCNulty, William E.
REGISTRATION NUMBER: 22,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 GVEYKVY 338
                                                                                                                                                                                                                                                                                                                                                                                  |: |: :
403 GMPYRSF 409
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DEWAICQIRTTANFATUNPFW-NWFCGGLNHQVTHHLFPNICHIHYPQLENIIKDVCQEF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GRVYDITRFLSEHPGGEEVLLEQAGADATESFEDVGHSPDAREMLKQYYIGDVHPNDLKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 137; DB 2; Length 104; Pred. No. 3.57e-02; 11; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08801972
Patent No. 5831018
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                           104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PAPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1217655
UENCE 104 AA; 11672 MW; 58506 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                              Sequence 5, Application US/08801972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 amino acids
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%;
Best Local Similarity 37.9%;
Matches 25; Conservative
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94304
                                                                       332 GVEYKVY 338
                                                                                                       403 GMPYRSF 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                          US-08-801-972-5
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                                                                     273 DEWAICQIRTTANFATNNPFW-NWFCGGLNHQVTHHLFPNICHIHYPQLENIIKDVCQEF 331
                                                                                           Gaps
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                                     3;
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08473508
Patent No. 5689050
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Nuccio, Michael
APPLICANT: Freyssinet, Georges L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
Score 155; DB 1; Length 359;
Pred. No. 1.67e-03;
16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 155; DB 1; Length 359;
Pred. No. 1.67e-03;
16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEE: Scully, Scott, Murphy & Presser P: 400 Garden City Plaza Garden City
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/473,508
FILING DATE: 07-JUN-1995
CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,382
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 359 AA; 41425 MW; 698417 CN;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (516) 742-4343
TELERAX: (516) 742-4366
TELERX: 230 901 SANS UR
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McNulty, William E. REGISTRATION NUMBER: 22,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 359 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KY: United States
11530
                                                                                                                                                                                                                                               STANDARD;
 Query Match 4.4%;
Best Local Similarity 32.8%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.4%;
Best Local Similarity 32.8%;
Matches 22; Conservative
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403 GMPYRSF 409
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US-08-473-508-2
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COUNTRY:
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Sequence 6, Application US/08624125
Patent No. 5743141
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCHEENING SUCH GENES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 PDLQHIPVFAVSTRL-FNSITSVFYGRVLKFDEVARFLVSYQHWTYYFVMIFGRVNLFIQ. 269
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Best Local Similarity 21.1%; Pred. No. 1.01e+01;
Matches 24; Conservative 36; Mismatches 44; Indels 10; Gaps
                                                     Sequence 2, Application US/08276099A
Patent No. 5591825
GENERAL INFORMATION:
APPLICANT: MCKNight, Steven L
APPLICANT: MCKNight, Steven L
APPLICANT: Hou, Jinzhao
TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: ADDRESCE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: ADDRESCE: ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: Galifornia
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 AFQHRSVSWSQFNKEI-LLGRGFTFWQWFDGVLDLTKRCLRSYWSDRLIIGFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,099A
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN: Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A 59451-1/RAO
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 AA
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MOLECULE TYPE: protein
JENCE 847 AA; 94134 WW; 3802900 CN;
Sequence 2, Application US/08276099A
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 847 amino acids
amino acid
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ID US-08-624-125-6

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DE Sequence 6, Appli
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CC Sequence 6, Appli
CC Sequence 7, Appli
CC Sequence 7, Appli
CC AppliCANT: CC APPLIC
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Pred. No. 1.01e+01;
36; Mismatches 44; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08781890
Patent No. 5710266
GENERAL INFORMATION:
APPLICANT: MCM.91ht, Steven L
APPLICANT: Hou, Jinzhao
TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
CORRESPONDENCE ADDRESS: ADDRESSE: FLERK HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 AFQHRSVSWSQFNKEI-LLGRGFTFWQWFDGVLDLTKRCLRSYWSDRLIIGFIS 543
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2IP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,099
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/CDOCKET NUMBER: A 59451-1/RAO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             847
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APPLICATION NUMBER: US/08/781,890
FILING DATE: 05-JAN-1997
CLASSIFICATION: 536
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SEQUENCE 847 AA; 94134 MW; 3802900 CN;
                                                                 PRT;
                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08781890
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15) 398-3249
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       847 amino acids
mino acid
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                                                                 STANDARD;
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Best Local Similarity 21.1%;
Matches 24; Conservative
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                   RESULT 12
ID US-08-781-890-2
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38 HHTPRKGVFELNDLFAV-VFAGVALALIAVGTAGVWPLQWIGCGMTVYGLLYFL-VHDGL 95
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                                       COMPUTER REALABLE FORM:
MEDIUW TYPE: FILIPOPY MISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION NUMBER: US/08/096,623A
FILING DATE: 09-DEC-1991
PRIOR APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 38-FEB-1991
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION NUMBER: US 07/552,551
FILING DATE: 18*MAY-1990
PRIOR APPLICATION NUMBER: US 07/525,551
FILING DATE: 18*MAY-1990
PRIOR APPLICATION NUMBER: US 07/555,551
FILING DATE: 18*MAY-1990
PRIOR APPLICATION NUMBER: US 07/487,613
FILING DATE: OF-MAR-1990
ATTONINY/AGENT INFORMATION:
WAND: AMERICATION NUMBER: US 07/487,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FENCE 176 AA; 19990 MW; 151305 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Thu Feb 18 11:38:43 1999 Job time: 27 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gamson, Edward P. REGISTRATION NUMBER: 29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: AM TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 655-1501 TELEFAX: (312) 655-1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |: :::||||:|:
158 VGHDSGHYQVMPTRGY-NRI 176
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                                 COMPUTER READABLE FORM:
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Patent No. 568438
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Blosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 NEMSRSGIFEKKGHHIMWTFVGVAVMMAAI-VYGVLASESVGVHMLCGALLGLLWIQAAY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 HHTPRKGVFELNDLFAV-VFAGVAIALIAVGTAGVWPLQWIGCGMTVYGLLYFL-VHDGL 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STAIE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%; Score 97; DB 1; Length 175; Best Local Similarity 28.8%; Pred. No. 2.17e+01; Matches 23; Conservative 22; Mismatches 30; Indels
                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/624,125

FILING DATE: 29-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 AA.
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120 S. Riverside Plaza, 22nd Floor
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JENCE 175 AA; 19867 MW; 149517 CN;
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                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELBER, SIEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECHANICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 V-HQRWPFHWIPRRGYLKRL 113
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158 VGHDSGHYQVMPTRGY-NRI 176
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TOPOLOGY: linear
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CITY: Chicago
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COUNTRY: USA
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US-08-096-623A-18
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Feb 18 11:39:01 1999; MasPar time 23.20 Seconds 733.938 Million cell updates/sec Run on:

lar output not generated.

>US-08-934-254-27 (1-452) from US08934254.pep 3515 1 MEGEAKKYITAEDLERHNKS......LNSAPCPKKLGYGEAYNTHG 452 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

321224 seqs, 37675139 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92 18:NEWP 19:NEWU8 20:NEWU9

Mean 36.598; Variance 169.128; scale 0.216 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	0.00e+00	1.16e-208	7.28e-181	9.39e-180	1.50e-178	1.50e-178	1.50e-178	1.50e-178	4.80e-128	1.12e-127	1.12e-127	1.12e-127	1.12e-127	1.77e-118	6.21e-79	2.65e-67	4.45e-58	1.07e-50	1.07e-50	1.07e-50	1.07e-50
			Applicati	Applicatio	Applicatio	Applicatio	Applicati	Applicati	A.	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicati	
		Description	Sequence 27,	Sequence 5,	Sequence 5,	Sequence 5,		16,	'n	16,	Sequence 4,	Sequence 9,	Sequence 9,	Sequence 8,	7	6	11,	Sequence 13,	Sequence 2,	Sequence 8,	Sequence 9,	Sequence 10,	Sequence 10,
SUMMARIES		DI	US-08-934'-	US-09-116-	US-60-110-	US-08-934-	US-08-834-	us-08-956-	US-08-833-	us-08-926-	US-60-110-	US-08-956-	us-08-956-	US-08-834-	US-08-834-	us-60-110-	US-60-110-	US-60-110-	US-60-110-	US-08-834-	US-08-834-	us-08-926-	us-08-956-
		DB	14	16	7	14	13	14	13	14	7	14	14	13	13	?	7	~	7	13	13	14	14
		Length	452	458	448	448	446	446	446	446	393	252	252	252	252	286	253	162	202	125	125	125	125
	% Query	Match	100.0	69.2	60.7	60.3	0.09	0.09	0.09	0.09	44.4	44.3	44.3	44.3	44.3	41.5	29.5	25.5	22.6	20.3	20.3	20.3	20.3
		Score	3515	2433	2133	2121	2108	2108	2108	2108	1561	1557	1557	1557	1557	1457	1025	897	795	713	713	713	713
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73 FHPGTAWKHLDKLFTGYH-LKDYQVSDISRDYRKLASEFAKAGMFEKKGHGVIYSLCFVS 131
                                                                                                                             132 LLLSACVYGVLYSGSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIG 191
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                              13 ADGKKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGQDVTDAFIA
                                                                                                                                                                                    NCITGISIAWWKWTHNAHHIACNSLDYDPDLQHLPMLAVSSKLFNSITSVFYGRQLTFDP
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GENERAL INFORMATION:
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Hitz, William D
APPLICANT: Cahoon, Rebecca E
TITLE OF INVENTION: MEMBRANE-BOUND DESATURASES
FILE REFERENCE: BB-1264-P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2133; DB 2; I
Pred. No. 7.28e-181;
105; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA.
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CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 5
LENGTH: 448
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448 AA; 51634 MW; 1109964 CN;
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Best Local Similarity 57.8%;
Matches 262; Conservative 1
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ID US-60-110-784-5
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                                                                                                                                                                                                                           121 VAVMMAAIVYGVLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLI 180
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                                                                                   1 MEGEAKKIITAEDLERHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAF
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                           Length 452;
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                           Score 3515; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 0;
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Pred. No. 1.16e-208;
92; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gorgone, Gina APPLICANT: Gorgone, Gina APPLICANT: Corley, Neil C. APPLICANT: Corley, Neil C. APPLICANT: Baughn, Mariah R. TITLE OF INVENTION: HUMAN CYTOCHROMES FILE REFERENCE: PF-0557 US CURRENT APPLICATION NUMBER: US/09/116,639 CURRENT FILING DATE: 1998-07-16 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTLRDAAVQARDLNSAPCPKKLGYGEAYNTHG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 1040729, GenBank
WUENCE 458 AA; 52231 MW; 1118207 CN;
51763 MW; 1074264 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: HELIANTHUS ANNUUS
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Local Similarity 66.7%;
hes 300; Conservative
                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 452; Conservative
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 AA;
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US-09-116-639-5
452
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LENGTH: 458
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                                                                                                                                                                                                                         239 FDSLSRFFVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPL 298
                                                                                                                                                                                                                                                                                                                                     299 LVSCLPNWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDIS 358
                                                                                                         179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08934254
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCFIMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
STATE: New York
COMPUTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 LRTLRNTALQARDITK-PLPKNLVW-EALHTHG 448
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ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEX: 23 991 SANS UR
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08934254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-934-254-5
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60.3%; Score 2121; DB 14; Length 448;

Query Match

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APPLICAT: KNUTZON, DEBORAH
APPLICANT: MUKERI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDERSS:
ADDERSSED: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
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                                                                                                                                                                                                                                                                                                                                       179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT 238 :|:||:|||:|||:||||||:|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 11 :|| 
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                                                                                         Gaps
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9
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Best Local Similarity 57.6%; Pred. No. 9.39e-180;
Matches 261; Conservative 105; Mismatches 81;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 LRTLRNTALQARDITK-PLPKNLVW-EALHTHG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08834033A
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RESULT 7
ID US-08-833-610-5
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OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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                                                                                                                                                                                                                                                                                                         Length 446;
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REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUTCATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
JENCE 446 AA; 51415 MW; 1102977 CN;
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GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
TITLE OF INVENTION: METHODS AND CONTILLE OF INVENTION: OF LONG CHAIN INUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08956985
                                                                                                   TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    STRANDEDNESS: not relevant
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61 VAFHPASTWKNLDKFFFGYY-LKDYSVSEVSKVYRKLVFEFSKMGLYDKKGH-IMFATLC 118
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPOTER: IBM PC compatible.
COMPOTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,985
FILING DATE: 24-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,033
FILING DATE: 11-APR-1997
ATONNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
RELEPRAKE/DOCKET NUMBER: 32,750
RELEPRAKE (650) 328-4400
TELEPRAKE: (650) 328-4400
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ENCE 446 AA; 51415 MW; 1102977.CN;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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IRTLRDAAVQARDLNSAPCPKKL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 FDSLSRFFVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VAFHPASTWKNLDKFFTGYY-LKDYSVSEVSKVYRKLVFEFSKMGLYDKKGH-IMFATLC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAF 60
                                                                                                                   APPLICANT: MURKERJI, PRADIP
APPLICANT: HUDNG, YUNG-SHENG
APPLICANT: HUDNG, YUNG-SHENG
APPLICANT: CHAUDHARY, SUNITA
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FAITY ACIDS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                        ADDRESSEE: RAE-VENTER LAW GROUD, P.C. STREET: 260 SHERIDAN AVE, P.O. BOX 60039 CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LE TYPE: peptide
446 AA; 51415 MW; 1102977 CN;
                                                                             Sequence 5, Application US/08833610 GENERAL INFORMATION:
                                                   Sequence 5, Application US/08833610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                       APPLICANT: KNUTZON, DEBORAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 446 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                USA
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APPLICANT: KNUTZON, DEBORAH
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPPWMDWFHGGLQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPY-NYASFSKANEMT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,985A
FILING DATE: 14-OCT-1997
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,033
FILING DATE: 11-APR-1997
PRIOR APPLICATION NUMBER: US 08/833,610
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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larity 57.8%; Pred. No. 1.50e-178;
Conservative 104; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE128.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: P.O. Box 60039
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FINCE 446 AA; 51415 MW; 1102977 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08956985A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08956985A
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420 IRTLRDAAVQARDLNSAPCPKKL 442
                                                                                                                                                                    LRTLRNTALQARDITK-PLPKNL 439
                                                                                                                                                                                                                                                                                              STANDARD;
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ZIP: 94306-0039
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Best Local Similarity
Matches 256; Conserv
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ID US-08-956-985A-16
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                         179 FAANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IAYHPGTAWQYLDRFFTGYY-VQDYSVSEMSKDYRRLVSEFSKWGLFKTPGKGVYCSIFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ME-EPKKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
1 MEGEAKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAF
                                                 FIAMLFAMSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGI
                                                                                            FDSLSRFFVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPL
                                                                                                                                                     299 LVSCLPNWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDIS
                                                                                                                                                                                       CPPWMDWFHGGLQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPY-NYASFSKANEMT
                VAFHPASTWKNLDKFFTGYY-LKDYSVSEVSKVYRKLVFEFSKMGLYDKKGH-IMFATLC
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                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/60110784
GENERAL INFORMATION:
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E
TILLE OF INVENTION: MEDRANE-BOUND DESATURASES
FILE REFERRICE: BB-1264-P1
CURRENT APPLICATION NUMBER: US/60/110,784
CURRENT FILING DATE: 1998-12-03
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                           393 AA
                                                                                                                                                                                                                                                                           PRT;
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IRTLRDAAVQARDLNSAPCPKKL 442
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Best Local Similarity 54.1%;
Matches 204; Conservative
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Sequence 9, Application US/08956985
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                            357
IAGNVIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMT 237
                        238 YDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYS
                                                                                                                         LLLSRLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNI
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONFINING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,985
FILING APPLICATION TAX:
APPLICATION NUMBER: US 08/834,033
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/833,610
FILING DATE: 11-APR-1997
ATTORNEY/AGENT: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.128.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
FRICE 252 AA; 28956 MW; 353818 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08956985
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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   359 TCPPWMDWFFGGLQFQL 375
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ID US-08-956-985-9
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241 FFGGLQFQLEHH 252
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USA
  STRANDEDNESS:
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TELEX: N,
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                                       SEQUENCE
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                                                                                    GISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARF 120
                                    1 GVLYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KNUTZON, DEBORAH
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
             0; Gaps
                                                                                                                                                                                    WPERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDW
Best Local Similarity 74.6%; Pred. No. 1.12e-127;
Matches 188; Conservative 36; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,985A
FILING DATE: 24-0CT-1997
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,033
FILING DATE: 11-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/833,610
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: RAE-VENTER, BARBARA
NAME: RAE-VENTER, BARBARA
NAME: RAE-VENTER, BARBARA
                                                                                                                                                                                                                                                                                                            252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE128.01US
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: P.O. Box 60039
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08956985A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          STANDARD;
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ZIP: 94306-0039
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US-08-956-985A-9
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Sequence 8, Application US/08834033A
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: MUKERJI, PRADIP
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNTA
APPLICANT: CHAUDHARY, SUNTA
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
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                                                                                                                                                                                                                61 GISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARF 120
                                                                                                                                                                                                                                                                                                      121 LVSYQHFTYYPVNCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPN 180
                                                                                                                                                                                                                                                                                                                                                                                        181 WPERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDW 240
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                                                                                                   44.3%; Score 1557; DB 14; Length 252; 74.6%; Pred. No. 1.12e-127;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
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               TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 252 AA; 28956 MW; 353818 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08834033A
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
not relevant
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hes 188; Conservative
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TELECOMMUNICATION INFORMATION
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APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKENI, PRADIP
APPLICANT: HURMOND, JENNIFER
APPLICANT: HORMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                   121 LVSYQHFTYYPVNCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPN 180
                                                                                                                                                                                                                           61 GISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARF 120
                                                                                                                                 1 GVLYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLT 60
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                                                                                           Length 252;
                                                                                        Score 1557; DB 13; Length 2:
Pred. No. 1.12e-127;
36; Mismatches 28; Indels
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APPLICATION NUMBER: US/08/834,655 FILING DATE: IJ-APR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                           252 AA
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REFERENCE/DOCKET NUMBER: CGNE.124.00US
                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 252 AA; 28956 MW; 353818 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                         not relevant
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 252 amino acids TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                        Query Match
Best Local Similarity 74.6%;
Matches 188; Conservative
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MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CANOON, Edgar B.
APPLICANT: CAHOON, Rebecca E.
TITLE OF INVENTION: MEMBRANE-BOUND DESATURASES
FILE REFERENCE: BB-1264-P1
CURRENT APPLICATION NUMBER: US/60/110,784
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 9
LENGTH: 286
                                                                                                                                                                                                              Score 1557; DB 13;
Pred. No. 1.12e-127;
                                                                                                                                                                                                                                                   36; Mismatches 28;
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Pred. No. 1.77e-118;
58; Mismatches 49;
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ORGANISM: Zea mays
OUENCE 286 AA; 32723 MW; 422187 CN;
                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
FENCE 252 AA; 28956 MW; 353818 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/60110784
                                                                                                                           not relevant
(650) 328-4400
(650) 328-4477
              TELERAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
                                                   7:
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Local Similarity 62.0%;
hes 176; Conservative
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Best Local Similarity 74.6%;
Matches 188; Conservative
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                                                  DHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFLISYQHWTFYPVMCIARINLL 120
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Pred. No. 6.21e-79;
46; Mismatches 49; Indels
                                                                                                                         241 LRKVAPAVRDLCKKHGLTYSAATFWG-ANVLTWKTLRAAALQAR 283
                                                                                                                                    Sequence 11, Application US/60110784
GENERAL INFORMATION:
APPLICANT: Kinney, Anthony J.
APPLICANT: Chhoon, Edgar B.
APPLICANT: Chhoon, Rebecca E
TILLE OF INVENTION: MEMBRANE-BOUND DESATURASES
FILE REFERENCE: BB-1264-P1
CURRENT APPLICATION NUMBER: US/60/110,784
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Word Version 7.0A
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253 AA; 28981 MW; 356946 CN;
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                                                                                                                                                                                       STANDARD;
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Best Local Similarity 57.2%;
Matches 131; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (206)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (252)
SEQUENCE 253 A8; 28
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NAME/KEY: UNSURE
LOCATION: (161)
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(166)
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ID US-60-110-784-11
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LENGTH: 253
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NAME/KEY: U
LOCATION:
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Feb 18 11:35:18 1999; MasPar time 18.91 Seconds 895.315 Million cell updates/sec Run on:

lar output not generated:

>US-08-934-254-27 (1-452) from US08934254.pep 3515 1 MEGEAKKYITAEDLRRHNKS......LNSAPCPKKLGYGEAYNTHG 452 Itle:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

116738 seqs, 37463448 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Mean 49.791; Variance 105.274; scale 0.473 Statistic Database:

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Prod) No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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S35228 S46306	\$35228 \$46306 \$63052 \$46307 \$47029 RDMUNH	S35228 S46306 S63052 S46307 S47029 RDMUNH RDTONH RA1667	S35228 S46306 S46305 S43052 S47029 S4100NH RDIONH RA11667 RDIONH RDBJNH RDBJNH RDBJNH	S35228 S46305 S46305 S46307 S47029 S47029 S41667 RDBJNH RD	535228 546306 546306 547029 547029 541667 641667 641667 6421667 6421667 6421667 643167 643167 643167 643167 643167 643167 6431
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3.75e-12	5.34e-12	7.61e-12	1.08e-11	1.08e-11	4.44e-11	3.12e-11	4.44e-11	7.20e-10	3.60e-10	2.02e-09	1.43e-09	2.02e-09	2.02e-09	2.85e-09	2.85e-09	2.85e-09	2.85e-09	2.85e-09	2:85e-09	7.93e-09	5.64e-09
nitrate reductase (NA	cytochrome b5, hepati	nitrate reductase (NA	cytochrome b5, solubl	Д	p2,	p2 -	b5,	b5,	ochr	cytochrome b5, hepati	cytochrome b5, micros	membrane-bound cytoch	cytochrome b5, micros	hypothetical protein							
RDBHNP	A41085	S51160	RDBHNS	RDBHNH	S19254	S07554	S52301	807959	JN0803	JN0316	S07964	CBRB5	CBH05	D24211	CBHUSE	JC5783	C24211	CBHU5	JC5782	CBBO5	S67453
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189	188	187	186	186	182	183	182	174	176	171	172	171	171	170	170	170	170	170	170	167	168
24	22	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

г	ω ∽		ß	##molecule_type mRNA ##residues 1-458 ##label SPE	##CTOSS TELEGREES EMBL:X8/14.5; NIL:glu40/28; FIU:glu40/29 FICATION #superfamily cytochrome b5 core homology	#domain cytochrome b5 core homology #label CB5 #length 458 #molecular-weight 52231 #checksum 8719	Ouery Match 69.2%; Score 2433; DB 2; Length 458; Best Local Similarity 66.7%; Pred. No. 0.00e+00; Matches 300; Conservative 92; Mismatches 54; Indels 4; Gaps 4;		GEAKKYITAEDLRRHNKSGDLWISIQGKYYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIA 62	FHPGTAWKHLDKLFTGYH-LKDYQVSDISRDYRKLASEFAKAGMFEKKGHGVIYSLCFVS 131	YHPGTAWRHLDPLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKGHHIMWTFVGVA 122	LLLSACVYGVLYSGSFWIHMLSGALLGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIG 191			NILTGISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTRENSITSVFYGRVLKFDE 242		VARFLVSYQHWTXYPVMIFGRVNLFIQTFLLLTRRDVPDRALNLMGIAVFWTWFPLFVS 302
RESULT ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors	#title	#accession ##statu	### ###	##CIOSS-1 CLASSIFICATION	16-90 SUMMARY	Query Ma Best Loc Matches	13	m	73	63	132	123	192	183	252	243
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312 RLPNWPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFEKQTRGTIDIACSS 371

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*Superfamily nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase homology; molybdopterin-binding domain homology electron transfer; FAD; flavoprotein; heme; homodimer; metalloprotein; molybdopterin; multifunctional enzyme; NAD; nitrate assimilation; oxidoreductase
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Wilkinson, J.Q.; Crawford, N.M.
Mol. Gen. Genet. (1993) 239:289-297
Identification and characterization of a chlorate-resistant mutant of Arabidopsis thaliana with mutations in both nitrate reductase structural genes NIA1 and NIA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new locus (NIA1) in Arabidopsis thaliana encoding nitrate
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                                                                                                                                                                                                                                                       #domain cytochrome b5 core homology #label CB5\
#domain cytochrome-b5 reductase homology #label CBR\
#binding_site molybdopterin (Cys) (covalent) #status
predicted
#length 881 #molecular-weight 99222 #checksum 5837
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##residues 525-917 ##label CHE1
##cross-references EMBL:X13434; NID:916402; PID:9930001
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##cross-references EMBL:219050; NID:922756; PID:922757
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#cross-references MUID:89091069
#accession S01640
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Plant Mol. Biol. (1995) 29:491-506
Identification of cDNA clones corresponding to two inducible
nitrate reductase genes in soybean: analysis in wild-type
and nr(1) mutant.
                                                                                                                                                                                                                                                                                                                           substrate-inducible nitrate reductase 2 - soybean (fragment)
#formal_name Glycine max #common_name soybean
14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
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Physiol. Plantarum (1991) 82:197-204
Cloning and expression of a gene encoding a root specific nitrate reductase in bean (Phaseolus vulgaris).
303 CLPNWPERFGFVLISFAVTAIQHVQFTLNHFSGDTYVGPPKGDNWFEKQTKGTIDITCPP 362
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#formal_name Phaseolus vulgaris #common_name kidney bear
22-Nov-1993 #sequence_revision 08-Sep-1995 #text_change
                                                                      WMDWFFGGLQFQLEHHLFPRLPRCHLRSISPICRELCKKYNLPYVSLSFYD-ANVTTLKT
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molybdopterin-binding domain homology
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#domain cytochrome-b5 reductase homology #label
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##experimental_source cv. Saxonia
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Pred. No. 4.72e-17;
16; Mismatches 26;
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##residues 1-88
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molybdopterin-binding domain homology chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron; metalloprotein; molybdenum; molybdopterin; NAD; nitrate assimilation; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, M.A.; Stobart, A.K.; Shewry, P.R.; Napier, J.A. Plant Mol. Biol. (1994) 25:527-537
Tobacco cytochrome b(5): cDNA isolation, expression analysis and in vitro protein targeting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lytochrome b5 - common tobacco #formal name Nicotiana tabacum #common_name common tobacco 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 08-sep-1997 S46306; S33157
                                                                                                                                                               #binding_site molybdopterin (Cys) (covalent) #status
predicted\
#disulfide_bonds interchain #status predicted\
#binding_site heme iron (His) (axial ligands) #status
                                                                                          #domain molybdopterin-binding domain homology #label
PMO\
                                                                                                                             #domain cytochrome b5 core homology #label CB5\
#domain cytochrome-b5 reductase homology #label CBR\
                                                                                                                                                                                                                                                                                                                                                                                                        541 MNTASKMYSISE-VRKHNTADSAWIIVHGHIYDCTRFLKDHPGGTDSILINAGTDCTEEF 599
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                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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SIFICATION #superfamily cytochrome b5; cytochrome b5 core homology
                                                                                                                                                                                                                                                                                                                                                                                                                           #binding_site NAD (Lys, Cys) #status predicted\
#binding_site FAD (Tyr) #status predicted
#length 917 #molecular-weight 103125 #checksum 2177
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                                                                                                                                                                                                                                                                                                                               Score 217; DB 2; Length 917; Pred. No. 1.44e-16;
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5.9%; Score 209; DB 2; Length 139
Best Local Similarity 41.8%; Pred. No. 2.74e-15;
Matches 33; Conservative 17; Mismatches 27; Indels
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##residues 1-139 ##label SMI
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Best Local Similarity 38.4%;
Matches 28; Conservative
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ORGANISM
DATE
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667-917
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SUMMARY
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##molecule_type DNA
##residues 1-120 ##label DEA
##cross-references EMEL:Z71387; NID:g1302031; PID:e239931; PID:g1302032;
##cross-references EMEL:Z71111C
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Tobacco cytochrome b(5): cDNA isolation, expression analysis and in vitro protein targeting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.; Valle, G. submitted to the EMBL Data Library. February 1996
The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number
                                                                                                                                                                                                                                                                                                           Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon,
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Cloning and characterization of a yeast cytochrome b
(5)-encoding gene which suppresses ketoconazole
hypersensitivity in a NADPH-P-450 reductase-deficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *superfamily cytochrome b5; cytochrome b5 core homology electron transfer; heme; transmembrane protein
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#domain transmembrane #status predicted #label TMM
#length 120 #molecular-weight 13297 #checksum 2403
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De Antoni, A.; D Angelo, M.; Dal Pero, F.; Sartorello,
Pandolfo, D.; Lanfranchi, G.; Valle, G.
submitted to the Protein Sequence Database, April 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-16,'Q',18-120 ##label TRU
##cross-references EMBL:L22494; NID:9431761; PID:9431762
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27-Jan-1995 #sequence_revision 27-Jan-1995 #
08-Sep-1997
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NCE S47919
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Best Local Similarity 38.7%;
Matches 29; Conservative
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$46306
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Clarkson, D.T. subth, A.J.; Prosser, I.M.; Forde, B.G.; submitted to the EMBL Data Library, July 1994 Cloning and characterization of the nitrate reductase gene in Lotus japonicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitrate reductase (NADH) (EC 1.6.6.1) nia - Lotus japonicus
#formal_mame Lotus japonicus
19.Mar-1997 #sequence_revision 19-Mar-1997 #text_change
20.Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nia
327/1; 374/1; 451/3
#superfamily nitrate reductase (NADH); cytochrome b5 core
homology; cytochrome-b5 reductase homology;
molybdopterin-binding domain homology
chromoprotein; electron transfer; FAD; flavoprotein; heme;
iron; metalloprotein; molybdenum; molybdopterin; NAD;
nitrate assimilation; oxidoreductase
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#domain cytochrome b5 reductase homology #label CBR\
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predicted\
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                                      ##residues 1-137 ##label SMI ##cross-references EMBL:X75670; NID:g414704; PID:g414705 CLASSIFICATION #superfamily cytochrome b5; cytochrome b5 core homology
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#binding_site NAD(P) (Lys, Cys) #status predicted\
#binding_site FAD (Tyr) #status predicted
#length 900 #molecular-weight 101420 #checksum 4574
                                                                                                                                                                                                                                                                                      1 MSNDNKKVYTLEEVAKHNSKDDCWLIIGGKVYNVSKFLEDHPGGDDVLLSSTGKDATDDF
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                                                                                                                             #domain cytochrome b5 core homology #label #length 137 #molecular-weight 15296 #checksum
                                                                                                                                                                                             Score 203; DB 2; Length 137; Pred. No. 2.44e-14; 13; Mismatches 33; Indels
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##experimental_source strain B-129; cultivar GIFU
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preliminary
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Best Local Similarity 40.5%;
Matches 32; Conservative
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Best Local Similarity 37.0%;
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                         ##molecule_type mRNA
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#description
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CLASSIFICATION
  ##status
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REFERENCE
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Crawford, N.M.; Smith, M.; Bellissimo, D.; Davis, R.W. Proc. Natl. Acad. Sci. U.S.A. (1988) 85:5006-5010 Sequence and nitrate regulation of the Arabidopsis thaliana mRNA encoding nitrate reductase, a metalloflavoprotein with three functional domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology; cytochrome bs reductase homology;
molybdopterin binding domain homology
chromoprotein; electron transfer; FAD; flavoprotein; heme;
homodimer; iron; metalloprotein; molybdenum; molybdopterin;
NAD; nitrate assimilation; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This enzyme catalyzes the reduction of nitrate to nitrite in cytoplasm; each chain contains one equivalent of FAD, heme iron, and molybdenum-pterin as prosthetic groups. This is a key enzyme involved in the first step of nitrate assimilation in plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new locus (NIA1) in Arabidopsis thaliana encoding nitrate
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                                                                                                                                                                      #formal_name Arabidopsis thaliana #common_name mouse-ear
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##residues 522-917 ##label CHE
##cross-references EMBL:X13435; NID:916403; PID:9930002
##cross-references EMBL:X13435; NID:916403; PID:9930002
##note the translation of the nucleotide sequence is not
                                                                                                                       nitrate reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis
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#binding_site FAD (Tyr) #status predicted
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Pred. No. 1.18e-14;
18; Mismatches 26;
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EMBO J. (1988) 7:3309-3314
                                                                                                #type complete
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#accession A31821
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#accession S01641
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US-08-934-254-27.rpr

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61 IAYHPGTAWRHLD 73
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Gene (1989) 85:371-88
Cloning and analysis of the tomato nitrate reductase-encoding
gene: protein domain structure and amino acid homologies in
                                                                                                                                                                                                                                                                                                                                                                       romoprotein; electron transfer; FAD; flavoprotein; heme;
homodimer; iron; metalloprotein; molybdenum; molybdopterin;
NAD; nitrate assimilation; oxidoreductase
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#binding_site FAD (Tyr) #status predicted
th 911 #molecular-weight 102452 #checksum 368
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JQ0373
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                                   61 IAYHPGTAWRHLD 73
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homodimer; iron; metalloprotein; molybdenum; molybdopterin;
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Plant Cell Physiol. (1991) 32:1031-1038
Sequence analysis of cloned cDNA and proteolytic fragments for nitrate reductase from Spinacia oleracea L.
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#binding_site heme iron (His) (axial ligands) #status
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#journal Plant Mol. Biol. (1990) 15:187-190
#title Nuclectide sequence of a spinach nitrate reductase CDNA.
#cross-references MUID:91355858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Spinacia oleracea #common_name spinach
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
#journal J. Biol. Chem: (1991) 266:23542-23547
#title The sequence of squash NADH:nitrate reductase and its relationship to the sequences of other flavoprotein oxidoreductases. A family of flavoprotein pyridine nucleotide cytochrome reductases.
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#domain cytochrome-b5 reductase homology #label
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Pred. No. 3.51e-14;
18; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAD; nitrate assimilation; oxidoreductase
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Local Similarity 37.0%;
Les 27; Conservative
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nitrate reductase (NAD(P)H) (EC 1.6.6.2) - European white birch #formal_name Betula pendula #common_name European white birch 30-Jun-1992 #text_change 20-Mar-1998
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                                                                                                                       ##molecule_type protein
##residues . 659-673;722-731;758-766;789-798;802-814;829-833;846-852;
853-858;859-864;874-879;904-914;916-926 ##label QUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douglas, P.; Morrice, N.; MacKintosh, C.
FEBS Lett. (1995) 377:113-117
Identification of a regulatory phosphorylation site in the
hinge 1 region of nitrate reductase from spinach (Spinacea
oleracea) leaves.
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#binding_site phosphate (Ser) (covalent) (by nitrate reductase-inactivating kinase) #status experimental\
#binding_site heme iron (His) (axial ligands) #status
Quinn, G.B.; Trimboli, A.J.; Prosser, I.M.; Barber, M.J. Arch. Biochem. Blophys. (1996) 327:151-160
Spectroscopic and kinetic properties of a recombinant form the flavin domain of spinach NADH:nitrate reductase.
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#domain cytochrome-b5 reductase homology #label CBR\
#binding_site molybdopterin (Cys) (covalent) #status
predicted\
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##residues 659-701 ##label FID
##note sequence extracted from NCBI backbone (NCBIP:79483)
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    #binding_site NAD (Lys, Cys) #status predicted\
    #binding_site FAD (Tyr) #status predicted
#length 926 #molecular-weight 103970 #checksum 1366
                                                                                                                                                                                                                                             Phytochemistry (1991) 30:3519-3523
Isolation and partial amino acid sequence of domains
nitrate reductase from spinach.
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##molecule_type protein
##residues 'A',533-564 ##label F12
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##residues 1-898 ##label FRI
##coss-references EMBL:X54097; NID:g17924; PID:g17925
##cross-references EMBL:X54097; NID:g17924; PID:g17925
##note the authors translated the codon CAC for residue 31 as
Arg and CGG for residue 32 as His
Arg and CGG for residue 32 as His
FFICATION #superfamily nitrate reductase (NADH); cytochrome b5 core
homology; cytochrome-b5 reductase homology;
molybdopterin-binding domain homology
chromoprotein; electron transfer; FAD; flavoprotein; heme;
homodimer; iron; metalloprotein; molybdopterin;
NAD; NADP; nitrate assimilation; oxidoreductase
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                                                    #authors Friemann, A.; Brinkmann, K.; Hachtel, W.
#journal Mol. Gen. Genet. (1991) 227-97-105
#title Sequence of a CDNA encoding the bi-specific NAD(P)H-nitrate reductase from the tree Betula pendula and identification of conserved protein regions.
#cross-references MUID:91260687
#accession S15959
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#disulfide_bonds interchain #status predicted\
#binding_site heme iron (His) (axial ligands) #status
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#domain cytochrome-b5 reductase homology #label CBR\
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    #binding_site NAD(P) (Lys, Cys) #status predicted\
    #binding_site FAD (Tyr) #status predicted
#length 898 #molecular-weight 101001 #checksum 9371
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CLASSIFICATION #superfamily cytochrome b5; cytochrome b5 core homology
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Best Local Similarity 34.2%;
Matches 25; Conservative
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REFERENCE
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US-08-934-254-27.rpr

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de Silvestris, M.; D'Arrigo, A.; Borgese, N.
FEBS Lett. (1995) 370:69-74

The targeting information of the mitochondrial outer membrane isoform of cytochrome b(5) is contained within the carboxyl-terminal region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytochrome b5, found attached to various hepatic cell membranes, is a major component of the electron transport system, catalyzing the NADH-linked desaturation of fatty acids in the endoplasmic reticulum. It may also be involved in the NADH-linked pathway of drug hydroxylation reactions catalyzed by cytochrome p450.
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#domain cytochrome b5 core homology #label CB5\
#binding_site heme iron (His) (axial ligands) #status
predicted predicted #molecular-weight 15221 #checksum 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA ##label DES 32-135 ##label DES ##residues_references GB:X96392; EMBL:S79339; NID:g1217654; PID:e225547; ##cross-references GB:X96392; EMBL:S79339; NID:g1217654; PID:g1217655
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                                                                                                                                                                                                          caribM #type complete
cytochrome b5, outer mitochondrial membrane - rat
#formal_name Rattus norvegicus #common_name Norway rat
04-Dec-1986 #sequence_revision 29-Aug-1997 #text_change
24-Oct-1997
A00173; S66501
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Two homologous cytochromes b-5 in a single cell.
#cross-references MUID:83182449
                    #domain cytochrome b5 core homology #label CB5
th 135 #molecular-weight 14869 #checksum 369
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                                                                                        Score 195; DB 2; Length 135;
                                                                                                                                  17; Mismatches 29; Indels
                                                                                                             Pred. No. 4.39e-13;
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##molecule_type protein
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nes 31; Conservative
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Search completed: Thu Feb 18 11:35:47 1999 Job time : 29 secs.

		(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular.Ltd

Thu Feb 18 17:54:20 1999; MasPar time 1707.01 Seconds 1334.208 Million cell updates/sec

n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch_nn

>US-08-934-254-26 (1-1702) from US08934254.seq 1702 lar output not generated. Description: Perfect Score:

N.A. Sequence:

TABLE default Scoring table:

Dbase 0; Query 0 .. STD Nmatch

2077918 seqs, 669069696 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-pending 1:P9 2:U6000 3:U6001 4:U6002A 5:U6002B 6:U6003A 7:U6003B 8:U6004A 9:U600B 10:U6005 11:U6006 12:U6007 13:U600B 14:U600BB 15:U600BC 16:U6009A 17:U6009B 18:U6010A 19:U6010B 20:U7 21:U80 22:U81A 23:U81B 24:U81C 25:U82A 26:U82B 27:U82C 28:U83A 29:U83B 30:U84A 31:U84B 32:U84C 33:U85 24:U86 35:U87A 36:U87B 37:U87C 38:U88B 40:U88C 41:U89D 42:U89A 43:U89B 44:U89C 45:U89D 46:U89E 47:U90A 48:U90B 49:U90C 50:U91A 51:U91B 52:U92 53:NEWP

Variance 3.383; scale 3.183 Mean 10.769; tatistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sac	Score	Query Match	Query Match Length DB	DB		Description	Pred. No.
1702 100	100	0	1702	43	US-08-934-	Sequence 26, Applicati	0.00e+00
	10.	H	1684	33	US-08-831-	Sequence 1, Applicatio	4.24e-178
	10.	Н	1684	39	US-08-831-	Sequence 1, Applicatio	4.24e-178
	10	-4	1685	43	US-08-934-	Sequence 4, Applicatio	4
	9.	_	291	14	ns-60-086-	Sequence 1966, Applica	2.32e-106
	6.5		276	14	ns-60-086-	Sequence 2042, Applica	7.87e-99
	6.1		267	15	US-60-089-	1341,	4
98 2.8	5.8		298	13	ns-60-080-	Sequence 1738, Applica	_
	8		304	15	-680-09-sn	4177,	_
	5.7		578	34	US-08-624-	Sequence 14, Applicati	1.14e-82
	5.7		578	33	us-08-269-		1.14e-82
	5.3		266	14	us-60-086-	325	4.52e-74

27.7 E E E E E E E E E E E E E E E E E E	1.99e- 2.01e- 1.57e- 1.57e-
nce 14, Applicatione 14, Applicatione 14, Applicatione 114, Applicatione 115, Applic	
466 - Sequence 689 - Sequence 680 - Sequence 680 - Sequence 646 - Sequence 645 - Sequence 645 - Sequence 646 - Sequence 647 - Sequence 647 - Sequence 646 - Sequence 647 - Sequence	17 - 45 - 40 -
333 343 353 353 353 353 353 353	4 US-08- 5 US-60- 8 US-09-
721 721 721 721 721 721 721 721	.5 33 .1 25 .1 39 .1 39
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ALIGNMENTS

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Sequence 26, Application US/08934254
Sequence 26, Application US/08934254
GENERAL INFORMATION:
GENERAL THOMAS TENDED THOMS
TITLE OF INVENTION:
FOUNDED TO SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Pressèr
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                      E: Scully, Scott, Murphy & Pressèr
400 Garden City Plaza
           BP.
T 1
US-08-934-254-26 STANDARD; DNA; UNC; 1702
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83833
TELECOMMUNICATION INFORMATION:
TELEFONE: (516) 742-4343
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
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                                                                                                        Score 1702; DB 43;
Pred. No. 0.00e+00;
0; Mismatches 0
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             TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: line bot
MOLECULE TYPE: DNA (genomic)
        LENGTH: 1702 base pairs
                                                                                   LOCATION: 48..1406
SEQUENCE 1702 BP; 358 A; 471
SEQUENCE CHARACTERISTICS
                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1702; Conservative
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           TTATTGATTAATTTTTGTTGTTGGTGTGTCTATAGCAAGTTTATAATACTGAGATATA
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US/08831575
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Sequence 1, Application US/088315
SEQUENCE INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Li, Zhongsen
TITLE OF INVENTION: AO OLECSI
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US-08-831-575-1
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E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
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US-08-831-570-1 STANDARD; DNA; UNC; 1684 BP.
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CORRESPONDENCE ADDRESS:
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New York
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Pred. No. 4.24e-178;
0; Mismatches 507; Indels
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LOCATION: 43..1387
SEQUENCE 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 OTHER.
                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BPLICATION NUMBER: US/08/831,575 FILING DATE: 09-APR-1997 CLASSIFICATION: 800
            CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                        LENGIH: 1684 base pairs
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Local Similarity 57.7%;
les 697; Conservative
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                                                                                                                                                                                                                                                                                                                      nucleic acid
  NUMBER OF SEQUENCES:
                                             Garden City
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                                                        New York
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                                                                   COUNTRY:
                                                        STATE:
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526 ATGACTCCGGCCATTACCAGGTGATGCCAACCCGTGGATACAACAGAATCACGCAACTCA 585
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APPLICANT: Nunberg, Andrew N.
APPLICANT: Beremand, Phillip D.
ITILE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
TITLE OF INVENTION: COMPOSITION
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US-08-934-254-4 STANDARD; DNA; UNC; 1685
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APPLICATION NUMBER: US/08/934,254
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CITY: Garden City
STATE: New York
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Pred. No. 4.24e-178;
0; Mismatches 507; Indels
                                                                                                                                                                                                                                                                                                                  LOCATION: 43..1387
SEQUENCE 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 OTHER.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
                                                                                   CILING DALL.

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REBERBENES/DOCKET NUMBER: 10545
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 57.7%;
Matches 697; Conservative
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877
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                                                                                                                                                                                                             938 ITGTITCITGTITGCCIAAITGGGGTGAAAGAATTAIGTTTGTIATTGCAAGITTATCAG
                                                                                                                         706 ccgrcrccaccccacrcrrcaacrccarcaccrccgrcrrcrargcccgagrccrgaaar
                                                                                                                                                                                                                                                                                      818 GTGCTGCTAGGCTCAATATGTATGTACAATCTCTCATAATGTTGTTGACCAAGAGAAATG
                                                                                                                                                                                                                                                                                                                                       826 TCTTCGGCCGAGTCAACCTCTTCATCCAGACCTTTTATTGCTCCTCACCAGGCGCGACG
                                                                                                                                                                                                                                                                                                                                                                                             878 IGTCCIATCGAGCTCAGGAACTCTTGGGATGCCTAGTGTTCTCGATTTGGTACCCGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                886 TCCCTGACCGCGCTCTAAACTTAATGGGTATCGCGGTTTTCTGGACGTGGTTCCCGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGACTCTTTATCAAGATTCTTTGTAAGTTATCAACATTGGACATTTTACCCTATTATGT
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Sequence 4, Application US/08934254
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID ITILE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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400 Garden City Plaza
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1239 AGAAACA 1245
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                                                                                                                                                                                                                                                                                                                                                                                      405
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                                                                                                                                                                                              46 CAATGGAGGCGAAGCTAAGAAGTATATCACGGCGGAGGACCTCCGCCGCCACAACAAGT 105
                                                                                                                                                                                                                  CCGGAGATCTATGGATCTCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAG 161
                                                                                                                                                                             42 CAATGGCTGCTCAAATCAAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAAC 101
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                        AGTITICTAAAATGGGTTTGTATGACAAAAAGGTCATATTATGTTTGCAACTTTGTGCT
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                                                                                                                                        Score 172; DB 43; Length 1685; Pred. No. 4.24e-178;
                                                                                                                                                           0; Mismatches 507; Indels
                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 OTHER.
         83832YXWVU
                         TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
 REGISTRATION NUMBER: 19,827
        REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.1%;
Best Local Similarity 57.7%;
Matches 697; Conservative
                                                                                  nucleic acid
                                                                                            both
                                                                                                     linear
                                                                                          STRANDEDNESS:
                                                                                                    TOPOLOGY:
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1179 ITCCCAAGATGCCTAGGAAACCTTAGGAAAATCTCGCCCTACGTGATCAGGATTATGCA 1238
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Sequence 1966, Application US/60086722
GENERAL INFORMATION:
APPLICANT: Laludi, Raghunath
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
826 TCTTCGGCCGAGTCAACCTCTTCATCCAGACCTTTTTATTGCTCCTCACCAGGCGCGACG
                                                                                                                                                                                                                                                                                                                                    GAAAGCCTAAAGGGAATAATTGGTTTGAGAAACAAACGGATGGGACACTTGACATTTCTT
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                                                                             TIGITICITGITIGCCIAATIGGGGTGAAAGAATIATGITIGTTATTGCAAGTTTATCAG
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-086-722-1966 STANDARD; DNA; UNC; 291
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ATTORNEY/AGENT INFORMATION:
NAME: CERRONDE, WICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PL-0017 P
TELECOMMUNICATION INFORMATION:
TELEPRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1966:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/60/086,72;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                APPLICANT: Lalgudi, Raghunath
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman Bradiey
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: CORN EMBRYO
NUMBER OF SEQUENCES: 8690
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           182 CATCCTGTGCTCTCCTTGGATGGATTGGTTCCACGGTGGCCTGCCAGTTCCAGATTGAGCA 241
                                                                                                                                                                                       62 CTTCACCATCTGCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGT 121
                                                                                                                                                                938 CCCGCTCTTCGTATCTTGTCTCCCGAACTGGCCTGAACGGTTCGGGTTCGTCCTCATCAG 997
                                                                                                                                            2 CCCGTTGCTGGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGTGCTTTTCAG 61
                                                                                                                        Gaps
                                                                                                Score 116; DB 14; Length 291;
Pred. No. 2.32e-106;
0; Mismatches 83; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
2IP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
`""WARE: Word Perfect 8.0 for Windows/MS-DOS 6.2
'""ARE: """ Nord Porfect 8.0 for Windows/MS-DOS 6.2
"""ARE: """ Nord Porfect 8.0 for Windows/MS-DOS 6.2
"""ARE: """ Nord Porfect 8.0 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                  1178 CCACTTGTTCCCTAGGCTGCCGCGTGGGCAGCTTAGGAAGATTGCGCC 1225
                                                                                                                                                                                                                                                                                                                      242 CCATCTGTTTCCCCNCCTACCTAGGTGCCACCTCCGTAAG-TTGCGCC 288
                                                     IMMEDIATE SOURCE:
CLONE: 700551823H1
SEQUENCE 291 BP; 47 A; 88 C; 80 G; 75 T; 1 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 317 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                     US-60-086-856-2042 STANDARD; DNA; UNC; 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PL-0016 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2042, Application US/60086856 Sequence 2042, Application US/60086856 GENERAL INFORMATION:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                Ouery Match 6.8%;
Best Local Similarity 70.8%;
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                           MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 CAAGGGCAATGACTGGTTTGAGAAGCAGACGGCAGGCACGCTCGACATCCTGTGCTCTCC 122
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                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                            Gaps
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Seguence 1341, Application US/60089804
Seguence 1341, Application US/60089804
Seguence 1341, Application US/60089804
SEDECANT: Stuve, Laura L.
APPLICANT: Gooding, Douglas H.
APPLICANT: Gooding, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED NUMBER OF SEQUENCES: 2470
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                          Score 110; DB 14; Length 276;
Pred. No. 7.87e-99;
0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 6.1/MS-DOS 6.2 software CURRENT APPLICATION DATA: APPLICATION NUMBER: US/60/089,804
                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 70026134911
SEQUENCE 276 BP; 49 A; 85 C; 74 G; 67 T; 1 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-089-804-1341 STANDARD; DNA; UNC; 267 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                         2042:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CERRONE, MICHAEL M. REGISTRATION NUMBER: 36,132
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 204
SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.4%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEREWITH
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SOFTWARE: Word Pe
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STATE: CA
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APPLICANT: Lalgudi, Raghunath
APPLICANT: Lalgudi, Raghunath
APPLICANT: Isly, Laura Y.
APPLICANT: Isly, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: CORN LEAVES
NUMBER OF SEQUENCES: 5534
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AIGGAITGGITCCAIGGCGCCTGCAGITCCAGAITGAGCACCAICIGITCCCCCGCCIG 120
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                                                                                                                                                                                                                                                                                                                                                                                               Length 267;
                                                                                                                                                                                                                                                                                                                                                                                               Score 103; DB 15; Length 26
Pred. No. 4.23e-90;
0; Mismatches 43; Indels
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JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/080,506
                TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1341:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 70118361941
SEQUENCE 267 BP; 48 A; 83 C; 81 G; 55 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .T 8
US-60-080-506-1738 STANDARD; DNA; UNC; 298
REFERENCE/DOCKET NUMBER: PL-0020 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1738, Application US/60080506 Sequence 1738, Application US/60080506 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: HEREWITH
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Best Local Similarity 77.2%;
Matches 146; Conservative
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CENERAL INFORMATION:
CENERAL INFORMATION:
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CHILLE OF INVENTION:
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MEDIUM TYPE: Diskette (3.5in, 1.44 Mb)
COMPUTER: IBM PC/XI/AT, IBM PS/2 or compatibles
OPERATING SYSTEM: Windows 95/NT
CUTRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/089,810
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CLONE: 700100371H1
SEQUENCE 298 BP; 56 A; 90 C; 82 G; 69 T; 1 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 13;
Pred. No. 6.63e-84;
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US-60-089-810-4177 STANDARD; DNA; UNC; 304 BP.
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NAME: Lavin Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 38-21(15395)A
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: PL-0007 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-055
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1738:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 base pairs
TYRE: nucleic acid
STRANDEDNESS: single
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(314) 737-6047
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Best Local Similarity 71.7%;
Matches 160; Conservative
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CLASSIFICATION:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                125 CAATGCTCACCACATCTCATGCAATAGTCTTGACTATGATCCTGATCTCCAGCACATACC 184
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                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                           698 GETATICGCCGTCTCCACCCGACTCTTCAACTCCATCACCTCGGTCTICTATGGCCGAGT
                                                                                                                                                                                                                                                                                                                                            Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KAVANNUGH PH.D., MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS PH.D., LEWIS T.
TITLE OF INVENTION: SIGNALLING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
                                                                                                                         R3+R5 drought stressed
                                                                                                                                                         LIBRARY: SOYMON028
CLONE: 701102270H1
SEQUENCE 304 BP; 72 A; 78 C; 66 G; 84 T; 4 OTHER.
                                                                                                                                                                                                     Score 98; DB 15;
Pred. No. 6.63e-84;
                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                T 10
US-08-624-190-14 STANDARD; DNA; UNC; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: 0, APPLICATION NUMBER: US/08/624,190 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1182.003 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08624190 Sequence 14, Application US/08624190 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GREEN, GRANT
REGISTRATION NUMBER: 31,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                    LENGTH: 304 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    uery Match 5.8%;
est Local Similarity 70.0%;
tches 168; Conservative
                                                                                                              ORGANISM: Glycine ma:
DEVELOPMENTAL STAGE:
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MEDIUM TYPE: Floppy
                                                                   CDNA
                                                                                                                                      root
                                               TOPOLOGY: linear MOLECULE TYPE: CDN/
                                                       linear
                                                                                                                                              IMMEDIATE SOURCE
                                                                                                 ORIGINAL SOURCE:
ORGANISM: Gly
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                                                                                        ANTI-SENSE: NO
                                                                                                                                     TISSUE TYPE:
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APPLICANT: KAVANAUGH PH.D., MICHAEL
APPLICANT: FOT PH.D., DAVID
APPLICANT: POT PH.D., LEWIS T.
APPLICANT: WILLIAMS PH.D., LEWIS T.
TITLE OF INVENTION: SHC-ASSOCIATED INOSITOL POLYPHOSPHATE 5-PHOSPHATASE
TITLE OF INVENTION: (SAPTASE)
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                        62 DGSDKYSHKKKSKNKVVTKKRKYVADSKKRGCMKNKHSDMTGTWNMGNAKKTSWSKGGKT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 RDDSADYHDYVGTDSKWKHSTSVTKTVAHTWNRVVAKHNRSHCTDNVKTGANTGNKGAVG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 VSMNGTSGVNSHTSGSKKRRNNYMNRAGDKKSNTHRTHWGDNYRVDTWATKKYADSHDTR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 VTSVSKNG-GTVDSGRČYATKTKSTKYHSSCSVK-SGNGSGVVKGTKKSDY-DHSKSSDS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 DSYGGCARATTYTHHGTGHGKTSGKTRKYDVKTRDSSGKTKSTSHDMKWVTSRACSGSS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 AATGAAGGCGTCGGTGGTCCTGGCCGCCAGA--CTGAGGAGCGGGACCTCGCCGCCG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 RKVHTATYRRTRDKYAYTKKATGMKYNSWCDRVWKSYVHVVCSYGSTSDMTSDHSVATAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 TNNYMGVGGMHVKTSDTAWSYDKDSGCRGSTGSKKSTANRGRTSRSDGKNAGDTDTKMNY 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TAGTAGTAGCCGGTGAAGAGCGGATCCAGATGCCGCCACGCCGTGCCCGG-GTGGTACGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 GSSSKARKDSKMRKCGSSVTKAADRGGGKVARRSTCSSSAGRAAGGDKSGKKTVSSAVAK 538
                                                                                                                                                                                                                                                                                                                                                                                                         3 SARVRISSRDSGRRVGANNMVSKSISSDKVKA-HGSHRSVIVKASGKMKVDVSGKKKSK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 CTCCGA-CGGACTCCGACGCCAGCACGACGATGCCGCCATCATGACGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%; Score 97; DB 34; Length 578; Best Local Similarity 12.2%; Pred. No. 1.14e-82; Matches 70; Conservative 281; Mismatches 210; Indels 12;
                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE 578 BP; 37 A; 11 C; 62 G; 65 T; 403 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 GGGTGCTCCGCCCCCCCGAGAGCAGTCGTAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        539 RKSRSNTTTRVKSAVHHSKGRDYRDNTHHGKHR 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 11
US-08-569-578-14 STANDARD; DNA; UNC; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08569578 Sequence 14, Application US/08569578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIRON CORPORATION
                                                     14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4560 HORTON STREET
510-601-2706
                                                                                                 LENGIH: 578 base pairs
TYPE: nucleic acid
                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                         510-655-3542
                                                                                                                                                                 single
                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
APPLICANT: KAVAN
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 45
                                                                                                                                                                                        TOPOLOGY:
                           TELEFAX:
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7T 12.
US-60-086-722-3256 STANDARD; DNA; UNC; 266 BP.
                                                                                                  Sequence 3256, Application US/60086722 Sequence 3256, Application US/60086722 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 266 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%;
ilarity 76.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
STREET: 3174 PORTER
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                 XXXXXX
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                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
5.7%; Score 97; DB 33; Length 578;
Best Local Similarity 12.2%; Pred. No. 1.14e-82;
Matches 70; Conservative 281; Mismatches 210; Indels 12; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 RKVHTATYRRTRDKYAYTKKATGMKYNSWCDRVWKSYVHVVCSYGSTSDMTSDHSVATAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 DSYGGCARATTYTHHGTGHGKTSGKTRKYDVKTRDSSGKTKSTSHDMKWVTSRACSGSS 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 RDDSADYHDYVGTDSKWKHSTSVTKTVAHTWNRVVAKHNRSHCTDNVKTGANTGNKGAVG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VSMNGTSGVNSHTSGSKKRRNNYMNRAGDKKSNTHRTHWGDNYRVDTWATKKYADSHDTR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CICCGA-CGGACICCGACGCCAGCACGCCGIAGACGATICCCGCCAICAIGACCGCAACG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 VISVSKNG-GIVDSGRCYATKIKSTKYHSSCSVK-SGNGSGVVKGTKKSDY-DHSKSSDS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 INNYMGVGGMHVKTSDTAWSYDKDSGCRGSTGSKKSTANRGRTSRSDGKNAGDTDTKMNY 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSSKARKDSKMRKCGSSVTKAADRGGGKVARRSTCSSSAGRAAGGDKSGKKTVSSAVAK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SARVRISSRDSGRRVGANNMVSKSISSSDKVKA-HGSHRSVTVKASGKMKVDVSGKKKSK 61
                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,578 FILING DATE: 08-DEC-1995 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION: NAME: GREEN, GRANT NAME: GREEN, GRANT NAME: 11.259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE 578 BP; 37 A; 11 C; 62 G; 65 T; 403 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTGCTCCGCCGCCCACCGAGAGCAGTCGTAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 RKSRSNTTTRVKSAVHHSKGRDYRDNTHHGKHR 571
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1182.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 510-601-2706
TELEFAX: 510-601-655-3542
INFORMATION FOR SEQ ID NO: 14:
                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
EMERYVILLE
                                      USA
                                                       94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                    COMPUTER:
                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
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APPLICANT: Lalgudi, Raghunath
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley
TITLE OF INVENTION: CORN EARS
NUMBER OF SEQUENCES: 7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCCATGGCGGCCTGCAGTTCCAGATTGAGCACCATCTGTTCCCCCGGCCTGCTCGGTGC-C 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1207 AGCITAGGAAGATIGCGCCCTIGGCTCGGGACTTGTGTAAGAAGCACGGGATGCCGTAT 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ACCITCGGAAGGIIGCGCCGGCGGTGCGIGACCIIIGCAAGAAGCAIGGGCIGACCIAI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90; DB 14; Length 266;
Pred. No. 4.52e-74;
0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 8.0 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/086,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: 700611205H1
SEQUENCE 266 BP; 47 A; 81 C; 83 G; 54 T; 1 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JT 13
US-08-466-194-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                           E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHABL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PL-0017 P
TELEPHONE: (650) 845-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3256:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/60/086,722
HEREWITH
                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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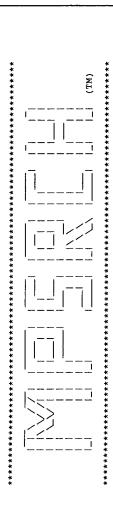
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APPLICANT: KAVANAUGH PH.D., MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS PH.D., LEWIS T.
TITLE OF INVENTION: IDENTIFICATION, CLONING, AND USE OF
TITLE OF INVENTION: SHC-ASSOCIATED INOSITOL POLYPHOSPHATE 5-PHOSPHATASE
TITLE OF INVENTION: (SAPTASE)
NUMBER OF SEQUENCES: 32
                        945 TICGTATCTTGTCTCCCGAACTGGCCTGAACGGTTCGGGTTCGTCCTCATCAGCTTTGCG 1004
                                                     934 GGTTCCCGCTCTTCGTATCTTGTCTCCCGAACTGGCCTGAACGGTTCGGGTTCGTCTCA 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886 TCCCTGACCGCGCTCTAAACGGTATCGCGGTTTTCTGGACGTGGTCCCGC-TC 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 VADSKKRGCMKNKHSDMTGTWNMGNAKKTSWSKGGKTRDDSADYH-DYVGTDSKWKHSTS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 VTKTVAHTWNRVVAKHNRSHCTDNVKTGANTGNKGAVGVSMNGTSGVNSHTSGSKKRRNN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 YMNRAGDKKSNTHRTHWGDNYRVDTWATKKYADSHDTRRKVHTATYRRTRDKYAYTKKAT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 KSTSSSDKVKAHGSHRSVTVKASGKMKVDVSGKKKSKDGSDKYSHKKKSKNKVVTKKRKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.2%; Score 89; DB 33; Length 578; Best Local Similarity 12.2%; Pred. No. 7.53e-73; Matches 66; Conservative 259; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/569,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE 578 BP; 37 A; 11 C; 62 G; 65 T; 403 OTHER.
                                                                                                                                                                                                                       UT 14
US-08-569-578-14 STANDARD; DNA; UNC; 578 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/569,578
08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1182.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08569578
Sequence 14, Application US/08569578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GREEN, GRANT
REGISTRATION NUMBER: 31,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-601-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                           1427 YYYYYYYG 1435
                                                                                                                                                        994 TCAGCTTTG 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94608
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                                                                                                                                                                                                                                                                 XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 CCCACAACGCCCACCACCTCGCCTGCAACAGCCTCGACTACGACCCCGGACCTCCAGCACA 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 874 CAGGCGCGCGTCCCTGACCGCGCTCTAATGGGTATCGCGGTTTTCTGGACGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 TCCCCGTATTCGCCGTCTCCACCGACTCTTCAACTCCATCACTCGGTCTTCTATGGCC
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,194
FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: US 08/232,463
FILING DATE: 22-APR-1994
PRIOR APPLICATION NUMBER: US 07/935,313
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: BP 91 114 300.6
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATONNEY/AGENT INPORMATION:
NAME: BENTY, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                     APPLICANT: SCHEIFLINGEN, ...
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, NW, Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB 31;
Pred. No. 2.70e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30472/201 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08466194
Sequence 14, Application US/08466194
                                                              DORNER, F.
SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                          GENERAL INFORMAT
APPLICANT: DOI
                                                                                                                                                                                                                                                                                                   20007
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1005 GICACGGCGATCCAGCACTTCACGCTCAACTACTACGGGGGACACATACGTG 1064
                                                                                                                           SGKTRKYDVKTRDSSG-KTKSTSHDMKWVTSRACSGSSTNNYMGVGGMHVKTSDTAWSYD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 ADRGGGKVARRSTCSSSAGRAAGGDKSGKKTVSSAVAKRKSRSNTTTRVKSAVHHSKGRD 560
                                                                                    264 GMKYNSWCDRVWKSYVHVVCSYGSTSDMTSDHSVATAGVTSVSKNGGTVDSGRCYATKTK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                          441 KDSGCRGSTGSKKSTANRGRTSRSDGKNAGDTDTKMNYGSSSKARKDSKMRKCGSSVTKA
                                                                                                                                                                                                      STKYHSSCSVKSGNGSGVVKGTKKSDYDHSKSSDSDSYGGCAR-ATTYTTH-HGTGHGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KAYANAGH PH.D., MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS PH.D., LEMIS T.
TITLE OF INVENTION: SIGNALLING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE 30
ADDRESSES: CHIRON CORPORATION
STREET: 4560 HORTON STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERALING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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US-08-624-190-14 STANDARD; DNA; UNC; 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08624190 Sequence 14, Application US/08624190 GENERAL INFORMATION:
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NAME: GREEN, GRANT
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 1182.
TELECOMMUNICATION INFORMATION:
TELEFAX: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE 578 BP; 37 A; 11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                        440
                                                                                                       826 TCTTCGGCCGAGTCAACCTCTTCATCCAGTACCTTTTTATTGCTCCTCACCGGGCGCGACG 885
                                                                                                                                                           85 VADSKKRGCMKNKHSDMTGTWNMGNAKKTSWSKGGKTRDDSADYH-DYVGTDSKWKHSTS 143
                                                                                                                                                                                  TCCCTGACCGCGCTCTAAACTTAAATGGGTATCGCGGGTTTTTCTGGACGTGGTTCCCGC-TC 944
                                                                                                                                                                                                                                        144 VIKIVAHIWNRVVAKHNRSHCIDNVKIGANIGNKGAVGVSMNGISGVNSHISGSKKRRNN 203
                                                                                                                                                                                                                                                                                                                                                                                                  264 GMKYNSWCDRVWKSYVHVVCSYGSTSDMTSDHSVATAGVTSVSKNGGTVDSGRCYATKTK 323
                                          Gaps
                                                                              KSTSSSDKVKAHGSHRSVTVKASGKMKVDVSGKKKSKDGSDKYSHKKKSKNKVVTKKRKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 YMNRAGDKKSNTHRTHWGDNYRVDTWATKKYADSHDTRRKVHTATYRRTRDKYAYTKKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 SCKTRKYDVKTRDSSG-KTKSTSHDMKWVTSRACSGSSTNNYMGVGCMHVKTSDTAWSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STKYHSSCSVKSGNGSGVVKGTKKSDYDHSKSSDSDSYGGCAR-ATTYTTH-HGTGHGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 ADRGGGKVARRSTCSSSAGRAAGGDKSGKKTVSSAVAKRKSRSNTTTRVKSAVHHSKGRD
                                          .
6
  Length 578;
Query Match 5.2%; Score 89; DB 34; Length 578 Best Local Similarity 12.2%; Pred. No. 7.53e-73; Matches 66; Conservative 259; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Thu Feb 18 18:55:18 1999 Job time : 3658 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Thu Feb 18 16:22:44 1999; MasPar time 2188.90 Seconds 1392.438 Million cell updates/sec ou:

lar output not generated. Title:

1 CCCCAAAAATTTTCATTGTT.......TTTTTGGTAAAAAAAAA 1702 GGGGTTTTTAAAAGTAACAA......AAAAAACCATTTTTTTTT >US-08-934-254-26 (1-1702) from US08934254.seq 1702 Description:
Perfect Score:
N.A. Sequence:
Comp:

Scoring table:

TABLE default Gap 6

Dbase 0; Query 0 •• Nmatch STD

Searched:

2275026 seqs, 895388244 bases x 2

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est56 Database:

Database:

5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17 14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est21 18:gb_est2 17:gb_est5 22:gb_est6 23:gb_est2 14:gb_est8 25:gb_est9 26:gb_gss1 27:gb_est6 28:gb_gss3 29:gb_gss4 1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est109

Mean 11.588; Variance 2.268; scale 5.110

stics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			•						
S O O	1111		Ollery						
	No.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No.	
	-	172	10.1	556	11	H36955	15084 Lambda-PRL2 Arab	3.966-283	
	7	156	9.2		디	W43255	22634 Lambda-PRL2 Arab	4.38e-250	
	m	142	8.3		11	T42806	6069 Lambda-PRL2 Arabi	2.18e-221	
	4	127	7.5		Ξ	T44542	7805 Lambda-PRL2 Arabi	6.45e-191	
	S	88	5.2	318	20	ATTS4723	A. thaliana transcribe	1.28e-113	
	9	64	3.8		1	N37558	18785 Lambda-PRL2 Arab		
	7	9	3.5		12	AA754459	97SN1787 Rice Immature		
O	∞	28	3.4		12	AA754459	97SN1787 Rice Immature		
U	σ	52	3.2		12	AA754458	97SN1784 Rice Immature	3.18e-52	
	10	51	3.0		Η	T42569	5832 Lambda-PRL2 Arabi	3.01e-45	
	11	20	2.9		16	T15209	crs698 Ricinus communi	1.59e-43	
	12	48	2.8		12	AA754458	97SN1784 Rice Immature	4.09e-40	
	13	46	2.7	2275	디	AF034173	Homo sapiens ntcon2 co	9.56e-37	

1. .556 //organism="Arabidopsis thaliana"
/strain="var columbia"
/strain="var columbia"
/strain="var columbia"
/note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7

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Query Match
                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m
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ORIGIN
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Matches
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1 (bases 1 to 408)

Newman,T., GeBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntossh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using /db_xref="taxon:3702"
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22634 Lambda-PRL2 Arabidopsis thaliana cDNA clone 249B14T7, mRNA
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                                                                                                                                                                                                                                    Score 172; DB 11; L. Pred. No. 3.96e-283; O; Mismatches 137;
                                                                                                                                                              /clone_lib="Lambda-PRL2"
126 c 119 g 172 t
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MSU-DOE Plant Research Laboratory
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Arabidopsis thaliana
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69.1%;
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/note="Vector: lambda Zip-Lox; Site_1: Sal, Site_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) fay germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta;
eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 480)
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Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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Pred. No. 4.38e-250;
0; Mismatches 113;
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/organism="Arabidopsis thaliana"
/strain="var columbia"
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103 c 84 g 11
                                               Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo dT primed cDNA.
/db_xref="taxon:3702"
/clone="249B14T7"
                                                                                                                                                                                   Location/Qualifiers
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Local Similarity 69.6%;
les 259; Conservative
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/clone="126F9T7"
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                                                  Arabidopsis thaliana
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Best Local Similarity 72.6%;
Matches 199; Conservative
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                                  thale cress.
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ORGANISM
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/strain="varabidopsis thaliana"
/strain="var columbia"
/note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a conA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
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7805 Lambda-PRL2 Arabidopsis thaliana cDNA clone 126F9T7, mRNA
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                                                                                                                                                                             Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
Lansing,Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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                                                                                                                                             On Jan 8, 1998 this sequence version replaced gi:947458.
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0
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Pred. No. 2.18e-221;
0; Mismatches 96; Indels
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107 c 112 q 13
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Location/Qualifiers
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Best Local Similarity 71.2%;
Matches 237; Conservative
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T44542
g2759339
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Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; eugliocytledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 455)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., Minncsh, L., Ohlzogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)

On Jan 8, 1998 this sequence version replaced gi:948824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="war columbia"
//strain="war columbia"
//note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The CDNA
inserts were directionally cloned with Sal-Not arms using
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DEFINITION A. thaliana transcribed sequence; clone YAY347; 5' end, mRNA
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Pred. No. 6.45e-191;
0; Mismatches 75;
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/organism="Arabidopsis thaliana"
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Michigan State University
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109 c 88 q 14
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Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
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                                                                                                                                         Moriis, P.C., Guerrier, D., Barbet, JC. and Giraudat, J.
Direct Submission
Submitsed (24-MR-1995) CNRS, GDR-1003 ACS, INRA, laboratoire de
Biologie Moleculaire, BP 27, 31326 Castanet-Tolosan cedex, France.
E-mail:gdr-svp@toulouse.inra.fr. On behalf of: CNRS, ISV-CNRS, BP
BEL 23 91198 Giffyvette, France.
E-mail:giraudat@trefle.isv.cnrs-gif.fr
2 (bases 1 to 318)
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18785 Lambda-PRL2 Arabidopsis thaliana cDNA clone 20508T7, mRNA
8equence.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Green siliques of A. thaliana ecotype columbia"
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                                                                   Arabidopsis thaliana
Bukaryotae, mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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Eukaryotae: Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 562)
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Pred. No. 1.28e-113;
0; Mismatches 105; Indels
                                       EST; expressed sequence tag; partial cDNA sequence.thale cress.
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                                                                                                                                                                                                                                                                                                         Cloning vector: Lambda ZAPII non-oriented; Physiological conditions: greenhouse plants.
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/db_xref="taxon:3702"
/clone="YAY347"
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Location/Qualifiers
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Best Local Similarity 64.3%;
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain-war columbia.
//strain-war columbia.
//note-wector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
same plants as 3 but aerial tissue (stems, flowers and
sliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
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                                                                                                                                                                                                                            Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 2.21e-68;
0; Mismatches 197; Indels
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/organism="Arabidopsis thaliana"
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/clone_lib="Lambda-PRL2"
| 141 c 128 g 15
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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Location/Qualifiers
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Best Local Similarity 57.3%;
Matches 270; Conservative
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Eukaryotae; Viridiplantae;
Embryophyta; Tracheophyta;
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1 (bases 1 to 247)
                                                                                                                                                                                                             Unpublished (1998)
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                                             Oryza sativa
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97SNI787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa CDNA clone 97SNI787, mRNA sequence.
AA754459
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AA754459
92801165
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
12 c 15 g 35 t 179 others
                                                                                                                                                                                        Charophyta/Embryophyta group;
seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsidi
Poales; Poaceae; Oryza.
1 (basea 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
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Pred. No. 3.94e-61;
109; Mismatches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Department of Cytogenetics
National Inst. of Agri. Sci. and Tech,
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"/cultivar="Milyang23"
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tches 25; Conservation
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                                                                                                                                                                       Oryza sativa
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ни/J4458 247 bp mRNA EST 20-JAN-1998
97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA clone 97SN1784, mRNA sequence.
92801164
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/clone="97SN1787"
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli Solr"
/lab_host="E. coli Solr"
21 c 35 t 179 others
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Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Charophyta/Embryophyta group;
seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                   Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel. 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                         Poales; Poaceae; Oryza.

1 (bases 1 to 252)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 MYBBIGCMICIMWCWBHYNTKCIASGWHISINYDVKSSINIWGVTBSYDKSMHGYWCSBB 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 RGCCCCBAWMTTSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDC-KNVNWSTMT-WGT 67
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Best Local Similarity 12.7%; Pred. No. 1.52e-57;
Matches 29; Conservative 121; Mismatches 72; Indels
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On Jan 8, 1998 this sequence version replaced gi:933288
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/cultivar="Milyang33".
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Rice Immature Seed Lambda 2APII cDNA Library'
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R. Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
                                                                                                      Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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5832 Lambda-PRL2 Arabidopsis thaliana cDNA clone 114C17T7, mRNA
sequence.
142569
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Arabidopsis thaliana
Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Seed plants; Magnoliophyta;
Embryophyta; Seed plants; Massicaceae; Arabidopsis.
eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 352)
1 (bases 1 to 352)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AHCRYTVBWYYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWB 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HWDCTMNTVWRGCCCCBAWMN-KHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 oth
                                                                                                                                                                                                                                                                          and Tech, RDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
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                                                                                                                                                                                                                                    Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="97SN1784"
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Local Similarity 14.9%;
                                                                                                                                                                                                         Contact: Eun
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MEDLINE
      AUTHORS
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castor bean clone=pcrs698 library=lambdaZAPST strain=Baker 296 vector=lambdaZAPII primer=T3 Rsitel=EcoR1 Rsite2=XhoI Poly(A)+ RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of lummature castor fruits. CDNA was synthesized and cloned into lambdaZAPII according to the instructions of the manufacturer (Stratagene): synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ATCCAGGGCAAGGTCTACGACTGCTCTCGGTGGGCGGCGGAGCACCCCGGCGGCGAGGTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ATTCAAGGCAAGGTCTACAACGTCTCCNATTGGATTAAAACTCATCCGGAGGCGACACG 63
Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DDE-PRL, Michigan State University,Plant Biology Bldg.,E.
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van de Loo.F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
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Pred. No. 3.01e-45;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ACCGCTTGGCACCATCTCGACCATCTTTTCACCGGTTACCAC 165
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                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/strain="var columbia"
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83 c 75 g 10
                                                                                                                                      Lansing,Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: 77
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Best Local Similarity 65.4%;
Matches 106; Conservative
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3'end with Xho I site."
/clone="g7SN1784"
/clone="g7SN1784"
/clone="libr"Rice Immature Seed Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458 92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Bondryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 247)

Mahn,B.H., Kim,N.Y., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               57 GAAGCTAAGAAGTATATCACGCGGAGGACCTCCGCCGCCACAACAAGTCCGGCGATCTC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GAAACAAAGAAGTACATTACAAAAGAAGTCTTGAAAAGCACAATAACCCTGGAGATCTC 207
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                                 St, Stanford, CA 94305
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                                                                                                                                                                                                                                     Length 597;
                                                                                                                                                                                                                                Score 50; DB 16; Length 597
Pred. No. 1.59e-43;
0; Mismatches 76; Indels
                                                                                                                                                                                others
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National Inst. of Agri. Sci. and Tech,
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                          /organism="Ricinus communis"
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                                                                                                                                                                              171
                Carnegie Institution
Carnegie Institution, 290 Panama
                                                  Tel: 4153251521
Email: crs@andrew.stanford.edu
                                                                                                                                       /clone="pcrs698"
/strain="Baker 296"
111 c 120 g
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                                                                                       Location/Qualifiers
Somerville CR
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Best Local Similarity 62.8%;
Matches 130; Conservative
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 Contact:
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2 [bases i to 2275)
Tripodis,N. and Ragoussis,J.
Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
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                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                          667 ICGACTACGACCCCGACCTCCAGCACATCCCCGTATTCGCCGTCTCCACCCGACTCTTCA 726
                                                                                                                                                                                                                                                                                                                                                            63 RYTVBWYYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAY 122
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                                                                                                                                                       Length 247;
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                                                                           169 others
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Pred. No. 9.56e-37;
83; Mismatches 50; Indels
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
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/lab_host="E. 21 g 34 t 169 otl
                                                                                                                                               2.8%; Score 48; DB 12; I
larity 15.1%; Pred. No. 4.09e-40;
Conservative 103; Mismatches 91;
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/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
a 619 c 470 g 599 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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Best Local Similarity 15.6%;
Matches 25; Conservative
                                                                                                                                                       Query Match 2.8%;
Best Local Similarity 15.1%;
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Job time : 4650 secs.
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539 LSA, Berkeley, CA 94720-3200, USA
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Email: httpd://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
Plate: 55 row: H column: 2
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High quality sequence stop: 366.
Location/Qualifiers
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                                                                                                             AI107749 448 bp mRNA EST 26-AUG-1998 GH05586.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH05586 5prime, mRNA sequence.
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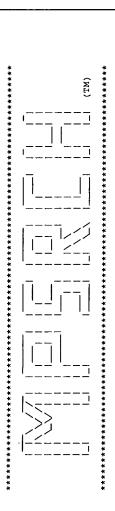
AI107703
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                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 448)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.

BDGP/HMI Drosophila EST Project
Unpublished (1997)
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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/sex="male and female"
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Pred. No. 1.05e-17;
0; Mismatches 51; Indels
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1612 WIKWI-IWWYMWSMIRWIMITYIIWWIWRIIKIWWWWWT 1650
                   pOT2. Plasmid cDNA library."
/db_xref="taxon:7227"
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/lab_host="DH5 - a]
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Drosophila melanogaster
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pst Local Similarity 62.5%;
tches 85; Conservative
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Email: httpd://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
Plate: 55 row: C column: 2
High quality sequence stop: 609.
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/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
terygota; Diptera; Brachycera; Muscomorpha; Ephydroidea
                 Drosophilidae; Drosophila.

1 (bases 1 to 613)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
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Pred. No. 1.05e-17;
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/lab_host="DH5 - al
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Best Local Similarity 62.5%;
Matches 85; Conservative
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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Thu Feb 18 17:50:01 1999; MasPar time 122.19 Seconds 1204.694 Million cell updates/sec

Tabular output not generated.

>US-08-934-254-26 (1-1702) from US08934254.seq 1702 Title:

Description: Perfect Score: N.A. Sequence:

Scoring table:

TABLE default Gap 6

165359 seqs, 43243793 bases x 2 Searched:

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Nmatch STD

Post-processing: Minimum Match 0% Listing first 45 summaries

n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1 Database:

Mean 9.108; Variance 5.151; scale 1.768 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

· SUMMARIES

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Pred. No.	5.25e-102	5.25e-10	5.86e-44	7.85e-14	3.99e-10	2.52e-08	9.86e-08	1.45e-06	1.16e-02	3.36e-03	1.16e-02	3.89e-02	1.28e-01	3.89e-02	3.89e-02	1.28e-01	1.28e-01	3.89e-02	1.28e-01	1.28e-01
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1010 0010 0 0 1 10 10 10 11 0 10 11 0 10 1		ALI NDARD; DNA; tion US/083 tion US/083 tion US/083 tion Will ss, Terry L ssinet, Geo erg, Andrew ON: DELTA ON: DELTA ON: DELTA UIJY, SCOCT UIJY, SCOCT UIJY, SCOCT EFORM: EFORM: EFORM: EFORM: EFORM: EFORM: TA TA TA TA TA TA TA TA TA T
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uuuuuuuuuu v.v.v.4.4.4.4.4.4.4		1 NEXA NEXA UENCE 4, APPLICA UENCE 4, APPLICA UENCE 4, APPLICA UENCE 4, APPLICA NERL INFORMATI APPLICANT: Red APPLICANT: Num APPLICANT: Free CONTRESPONDENCE ADDRESSE: SOUR CONTRY: Garden STATE: New Y. CONTRY: Uni ZID: 11530 COMPUTER: DA COMPUTER: PA COMPUTER: PA COMPUTER: PA COMPUTER: PA APPLICATION FILING DATE: CLASSIFICATION FILLERA APPLICATION FILLERA APPLICATION FILLERA ATTORNEY AGEN TELEFRONE: (51 TELEFRO
222222222222222222222222222222222222222		T 1 US-08-366-779-4 STANDARD; DNA; US-XXXXX Sequence 4, Application US/0836 APPLICANT: Thomas, Terry L. APPLICANT: Reddy, Avutu S. APPLICANT: Nunberg, Andrew TITLE OF INVENTION: PRODUCT TITLE OF INVENTION: PRODUCT TITLE OF INVENTION: PRODUCT TITLE OF INVENTION: PRODUCT TITLE OF INVENTION: PRELNA ADDRESSEE: 25 CORRESPONDENCE SCALLY, SCOCT, STREET: A00 Garden City P CITY: Garden City STREET: New York COUNTRY: United States ZIP: 11530 COMPUTER: IBM PC COMPATION STATE: New YORK COMPUTER: IBM PC COMPATION SOFTWARE: PATENTIN NUMBER: US/08 FILING DATE: 30-DEC-1994 CLASSIFICATION NUMBER: US/08 TELEPRONE STATE: 30-DEC-1994 TELEPRONE STATE: 30-DEC-1936 TELEPRONE (516) 742-4436 TELEPRONE (516) 742-4436 TELEERX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 4: SEGUENCE CHARACTERISTS: LENGTH: 1685 base pairs TYPE: nucleic acid
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                                             Length 1685;
                                          Score 172; DB 1; Length 168
Pred. No. 5.25e-102;
0; Mismatches 507; Indels
               MOLECULE TYPE: DNA (genomic)
SEQUENCE 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 OTHER
                                          Ouery Match 10.1%;
Best Local Similarity 57.7%;
Matches 697; Conservative
STRANDEDNESS: both
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SEQUENCE 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 OTHER.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
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400 Garden City Plaza
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APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freyssinet, Georges L.
APPLICANT: Freyssinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA I.
TITLE OF INVENTION: DELTA 6-DESATURASE
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
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US-08-789-936-4 STANDARD; DNA; UNC; 1685
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APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
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Sequence 4, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
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REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 813
TELECOMMUNICATION INFORMATION:
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TELEFAX: (516) 742-4366
TELEX: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 1685 base pairs
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COUNTRY: United
ZIP: 11530
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REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
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US-08-232-463-14 STANDARD; DNA; UNC; 7218
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                       Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOR NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 0.3%;
Matches 1; Conservative
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COMPUTER READABLE FORM:
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                                                                                                          102 CCGGAGATCTATGGATCTCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAG 161
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                                                     42 CAATGGCTGCTCAAATCAAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAAC 101
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 Score 172; DB 3; Length 1685; Pred. No. 5.25e-102;
                           0; Mismatches 507; Indels
Query Match
Best Local Similarity 57.7%;
Matches 697; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: FOWLPOX VIRUS

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Length 965;

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104 GTCCGGCGATCTCTGGATCTCCATCCAGGCCAAGGTCTACGACTGCTCTCGGTGGGCGGC 163
                                                                                                                                                                                                                                                         846 VTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTT 905
                                                                                                                                                                                                                                                                                 786 VHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMADTSSNSRSS 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 965;
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Pred. No. 3.99e-10;
77; Mismatches 67; Indels
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant Human Anti-Lewis TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/388,672A FILING DATE: 14-FEB-1995
                                                                                                          No. 7.85e-14;
                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP
                                                                                                                                76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                          221 CGCCTTCATTGCGTACCACCCGGGCACGG 249
                                                                                        Score 46;
                                                                                                                                                                                                                                                                                                                                             906 HGNGNTYYWYKGKAKYRVSNRSGVSRSGS 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIK: LOCAL
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 GENERAL INFORMATION:

APPLICANT: Wallace, T. Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man
REGISTRATION NUMBER: 30,946
                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wallace, T. Paul
Harris, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Felfe and Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harris, William APPLICANT: Carr, Frank J. APPLICANT: Old, Lloyd J. APPLICANT: Welt, Sydney APPLICANT: Kitamura, Kunio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 965 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                       Local Similarity 17.4%;
les 26; Conservative
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Best Local Similarity 17.1%;
Matches 30; Conservative
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ADDRESSE: Felfe and
STREET: 805 Third Av
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: U.S.A.
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STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                        Query Match
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                                                                                                                             Matches
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                                                           634 CCCACAACCCCACCACCTCGCCTGCAACAGCCTCGACTACGACCCCGACCTCCAGCACA 693
                                                                                        694 TCCCCGTATTCGCCGTCTCCACCCGACTCTTCAACTCCATCACTCGGTCTTCTATGGCC 753
                                                                                                                                                                          754 GAGTCCTGAAATTCGACGAAGTGGCACGGTTCCTAGTCAGCTACCAGCACTACT 813
                                                                                                                                                                                                                                                                814 ACCGGGCATGATCTTCGGCCGAGTCAACCTCTTCATCCAGACCTTTTATTGCTCCTCA 873
                                                                                                                                                                                                                                                                                                                                                    874 CCAGGCGCACCTCCCTGACCGCTCTAAACTTAATGGGTATCGCGGTTTTCTGGACGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                 934 GGTICCCGCTCTTCGTATCTTGTCTCCCGAACTGGCCTGAACGGTTCGGGTTCGTCCTCA 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wallace, T. Paul
APPLICANT: Harris, William J.
APPLICANT: Carr, Frank J.
APPLICANT: Old, Iloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
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APPLICATION NUMBER: US/08/388.6723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/388,672A
FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUD 5409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 PATENT NO. 5795961 APPLICANT: Wallace, T. Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe and Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               965 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 965 LENGIH: 975 mvpE: nucleic acid
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STRANDEDNESS:
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NAME/KEY: misc_feature
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776 GGTKKGURHUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTM 835
            836 ADTSSNSRSSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGD 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                       896 RVTTCRSSTIHGNGNIYYWYKGKAKYRVSNRSGVSRSGSGSGTDYTISSDATYYC 950
                                                                                                    CLONE: PTZgpt-Fls
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7218;
                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 n.
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2%; Score 37; DB 2; Len 0.8%; Pred. No. 2.52e-08; ative 197; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                     US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP
                                                                                                                                                                                                                                                                                   STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991 ATTONEN/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                       Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                            Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line IMMEDIATE SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                   XXXXXX
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APPLICANT: FOWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
1376 CCCAAGTITCTTAGGGCACGGGGCCGAATTAAGGICACGCGCCTGAACCGCCGCACCCT 1317
                                                                                         1136 CCACGGTGGGCACGTGATATCGATCGTCCCTTTTCGTCTCCTTCTCGAACCAGTTGTCGCC 1077
                                                                                                                                                                                                                                                                                                                     1196 CAGCCTAGGGAACAAGTGGTGCTCCAACTGGAACTGCAGCCCACCAAAGAACCAGTCCAT 1137
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-May-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
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Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 base pairs
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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ZIP: 94105-1493
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                                                                                                                                                                                                                                           45 DIDITIRNUNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTS 104
                                                                                                                                                                                                                                                                                                            105 SSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 GAGGTCGGGGTCGTAGTCGAGGCTGTTGCAGGCGAGGTGGTGGGCGTTGTGGGGTCCACTT 627
                                                                                                                                                                  Gaps
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    ö
  LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                  Length 215;
                                                                                                                                                                  67; Indels
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                                                                                                                  Score 34; DB 1; L
Pred. No. 1.45e-06;
60; Mismatches 67
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Pred. No. 1.16e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 9
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILLIO DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   165 ADGKVGSKNNGDRNNRYGTGTKSNVS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 512
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
                                                                                                                  7.0%;
Local Similarity 13.0%;
Local Similarity 13.0%;
Local 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.6%;
Best Local Similarity 10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                      Query Match
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                                                                                                                                                                  Matches
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CC Batent No. 5569830
CC GENERAL INFORMATION:
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
APPLICANT: POWELL, Ann
CC ATILLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC ATILLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC ATILLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC ATILLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC STREEP: Townsend and Townsend Khourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC STREET: California
CC STREET: CALIFORNIA
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955 CAAGATACGAAGAGGGGGAACCACGTCCAGAAAACCGGGGAAACCACTTAAGAGGG 896
                                                                                                                                                                                                                                                                                                          70 GNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGT-DGNRSGADSYGSSKTAMT 128
                                                                                                                                                                                                                                                                                                                                     129 SRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSN 188
                                                                                                                                                                                                                10 SVVSRTASCUDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYG 69
                                                                                                                                                                  Gaps
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean.".
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                    Length 215;
                                                                                                                                                                85; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                  Score 36; DB 1; L. Pred. No. 9.86e-08; 69; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTATION NUMBER: 34,774
REPERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
ELLING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                  Match 2.1%;
Local Similarity 16.7%;
les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94105-1493
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                                                                                                                    Query Match
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1381 CCATACCCAAGTTTCTTAGGGCACGGGCCGAATTAAGGTCACGCGCCTGAACCGCGCGA 1322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1441 AAGAAGATCCTCCAACCCAAAACACAAAACCACAATCAACCATGGGTGTTATAAGCTTCC 1382
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: METHODS OF STIMULATING PHAGOCYTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 2; Length 242; Pred. No. 1.16e-02; 41; Mismatches 141; Indels
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,846
FILING DATE: 12-JUL-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
SEQUENCE 290 BP; 17 A; 34 C; 8 G; 11 T; 220 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 12
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                  ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 555-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1261 GGCATCCCGTGCTTCTTACACAGTCC 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ROMON ** * CALLEDFROMCCRFAPPSC 207
                                                                                                                                                                                                                                                                                                                                                                 32,955
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.6%;
Best Local Similarity 11.6%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                     CORRESPONDENCE ADDRESS:
                    NUMBER OF SEQUENCES:
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STREET: 11
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Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: CYTOGEN COMPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 4; Length 81;
Pred. No. 3.36e-03;
20; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/11934 FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101-196-228
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US-08-273-846-1 STANDARD; DNA; UNC; 290 BP
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRIE: New York
COUNTRY: USA
                                                                                                        7T 10
PCT-US95-11934-92 STANDARD; DNA; UNC; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/08273846
Patent No. 5641863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAWE: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SCHREIBER, ALAN D.
APPLICANT: PARK, JONG-GU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uvery Match 1.6%;
Best Local Similarity 12.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                         : : ||||
626 CCACCACGC 618
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                63 BNNBNACGC 71
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                                                                                                                                                                                   Seguence
                                                                                                                                                                                                    Sequence
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Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
NUMBER OF ENQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                              Score 25; DB 4; Length 74; Pred. No. 1.28e-01; 20; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: INDEPT WILD.
COMPUTER: IND.
COMPUTER: DESCRIPTION OF STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin NaTA:
APPLICATION NUMBER: PCT/US95/11934
FILLIG DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
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SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7T 14
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELERAX: (212) 790-909
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                   INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTER.STICS: LENGTH: 74 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                            1.5%;
Similarity 9.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.5%;
Best Local Similarity 9.0%;
Matches 6; Conservative
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EDNESS: single
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   66141 PENNIE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   61 NNVNNAC 67
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TELEX:
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TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDEME ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 74;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 4; L
Pred. No. 3.89e-02;
20; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 13
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP
                                                                                                                                                                                                                                  1101-196-228
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Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
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FILING DATE: 20-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-7
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                  20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITORNEY/AGENT INFORMATION:
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larity 8.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                       74 base pairs
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conser
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                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 CCGACGCC 224
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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670 TCGAGGCTGTTGCAGGCGAGGTGGTGGGGTTGTGGGGTCCACTTCCACCACGCGATGCTG 611
                                                                                                                                                            Sequence 92, Application PC/TUS9511934
Sequence 92, Application PC/TUS9511934
Sequence 92, Application PC/TUS9511934
CENTERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: Elab PC compatible
COMPUTER: Elab PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: PCT/US95/11934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                                                       T 15
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/COCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELERAX: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                          610 ATTCCGG 604
                            61 NNBNNBG 67
                                                                                                                                      XXXXXX
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Score 26; DB 4; Length 81; Pred. No. 3.89e-02; 20; Mismatches 42; Indels Query Match 1.5%; Best Local Similarity 8.8%; Matches 6; Conservative

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Search completed: Thu Feb 18 17:54:01 1999 Job time: 240 secs.